

**FIGURE 1**

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA  
 CCTGGTGCACCCACCACC**ATGTT**TGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG  
 GTTTTCCACCCAGCTTTCACCAAGGCCTCCCTGTGTGAAGAATTCCATCACGAAGAATCA  
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA  
 GAACCTGGCCAAAGAACTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAATATTTAAAAAT  
 GATCAGATGGGAAGATGGTTTGTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTTGTGCTA  
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT  
 ATGTCAAGGATAGAATTCATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAACAGCT  
 TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACTTCATGATGAGAGGCTCTTG  
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC  
 CATATGACCAGAGCCAGGCCAAAGCATCTTGCTTGGTTGCTACATTTCTGGTGTGATGGGT  
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC  
 AGCTGGCATGTGGGAGGCCCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAGTTTCTGA  
 ACATGGGTGCACCCCTGGGAGTGGGCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG  
 TTTCTTCCACCTACCCCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT  
 AGTTCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT  
 CACCAATGTATGGAGTTCAAATAATGATCCATTAACTCGATGCTGAGTATCTACATGGAT  
 ACATTAATATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**tg**  
**AA**GTGACTCAGCTTCTGGCTTCTCTGCTACATCAATATCTTGTTTAAATGGGCGAGATATGC  
 ATTAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCAATATA  
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGCTCGCCTTTTTTCTGGAGAATAAATGCAGT  
 AATCCTCTCCCAATAAGCACACACATTTCAATTCTCATGTTTGAGTGATTTTAAATGTT  
 TTGGTGAATGTGAAAACATAAGTTTGTGTGATGAGAATGTAAGTCTTTTTTCTACTTTAAAAA  
 TTTAGTAGGTTCACTGAGTAACATAAAATTTAGCAAACTGTGTTGCATATTTTTTGGAGT  
 GCAGAATATGTAAATTAATGTCATAAGTGATTGGAGCTTTGGTAAAGGACCAGAGAGAAG  
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA  
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGAAACAAAGTGGTCATTGTTACATTCATTT  
 GCTGAACCTTAACAAAACGTTCATCTGAAACAGGCACAGGTGATGCATTTCTCTGCTGTG  
 CTTCTCAGTGCTCTCTTTTCAATATAGATGTGGTCAATGTTTGACTTGTACAGAATGTTTAATC  
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAAATGTTACAAAAGGAA  
 ATAACCTTTAAACATATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTTGCTTTTCCAG  
 AATACAAACAGTATACTCATG

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**FIGURE 2**

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL  
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI  
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP  
GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL  
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGVLVFSMFLLYDTQKVIKRAEVSPMYGV  
QKYDPINSMLSIYMDTLNIFMRVATMLATGGRKK

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**FIGURE 3**

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCCGTCTCCGCCCTTCTGCAT  
CGCGGGCTTCGGCGGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGGCCGCGTTCGTGAGGG  
GTTCGGCAGCGGGAGTCGGCGGGCTTGTGCATCTTGGCTACCTTGGGTTCGAAGATGTCCGG  
ACATCGGAGACTGGTTTCAGGAGCATCCCGCGCATCACGCGCTATTGGTTCGCCGCCACCGCTC  
GCCGTGCCCTTTGGTCGGCAAACTCGGCCCTCATCAGCCCGGCCATCCTTCCCTCTGGCCCGGA  
AGCCTTCCTTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGGT  
GTCCAGGAACCTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTTCTACGCGGA  
CTTGAACAGGAGCTTTTATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG  
GATTTGTCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA  
TGTTCAGTACTTTATGCTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA  
ACACGATTTAAGGCCCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG  
CTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTTCCTAATGTTCA  
GATACCCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCCGCTGG  
CTGCCCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC  
TGCTGATCAGAATGGCGGAGGCGGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC  
AGTGAAGGGGCGGCCCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCTCCAGTGTGGGTG  
CACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC  
GACTACGAGCAAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCCCAAGATTTTACAGAT  
TCTCATTTAGAGTCCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAAATGCAAACTGCAC  
TACATTTTGGGTGCTTCTCTTCTCCCCCTTCCGCTGCAATTAATGGGTTTTCAGGGGTCTCT  
AACTCTTGGGCTGTGAGCTGGGGCTGGGTCACCAAAACCTTCCCAAAGGACCTTATCTCTT  
TCTTGCACACATGCGCTCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG  
CCATAAAATTTGCTCTGCCCTTGACAGGTTCTGTTATTTATTTGACTTTTGGCAAGGCTGGTC  
ACAACAATCATATTTACGCTTATTTTCCCTTTTGGTGGCAGAACTGTACCAATAGGGGGAG  
AAGCAGGCCACGGATGAAGCGTTTTCTCAGCTTTTGGGAATTGCTTCAGTGCATGCTTGTGT  
AAGCGTTTGGCACTCTTCAGATATTTTTTATAAAAAAGTACCACGTGAGTTTCATGAGGGCCA  
CAGATTTGGTTATTAATGAGATACGAGGTTGGTGTGGGTGTTTGGTTTCCGTGAGCTAAGTGA  
TCAAGACTGTAGTGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC  
TTTGGCTTTTATATGATAGCCCTACTGGCTTGTGTAGCTGGAGTGTGGGTTGGCTTTGTGT  
TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG  
ATTCCCATTTCAATCTCATTCTGGATATGTGTTCAATTGAGTAAAGGAGGAGAGACCCCTCATA  
CGCTATTTAAATGTCACCTTTTTTGCCTATCCCCCGTTTTTGGTGTGTTTCAATTAATTTGT  
GAGGAAGGCGAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAAGCACATCTA  
AGGGAATAAATGATTTAAGGTTGAATGGCTTTAGAATCATTTGGGTTTTCAGGGGTGTGTTA  
TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACAGCTTAAATACCCACACCTTTTTT  
TCGTAGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCA  
TGGCTTTTTACACAGTTATTTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT  
ATTGAGTGGCTGTACACACTTTGAGGCAACTAAAAAGGCTTCAAACTGTTTGTATGATGATGAT  
TTTCAGGAACATTTGTGCTTAACAGTATGACTATTTCTTCCCACTCTTTAAACAGTGTGAT  
GTGTGTTATCTTAGGAAATGAGAGTTGGCAACAACTTCTCATTTTGAATAGAGTTTGTGTG  
TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGAGAGCTGAACCTTCACTGTCA  
TGTTTTGTTGTTTCATCTGCGCCACATAAAGTTTTTACTTGTAAAAATTTAGAGGCCATTA  
CCTAATATGTTGACGTACACTCATTTGTACAGGCGTGAGAGCTCATTTGTATGTATGAAGAA  
TTTCTGACAGTGGAGTACCGGAGTCTCTGGTGTACCCCTTTACAGCTAGCTGCGCTCGGAG  
CAGTCAATTTTTTCTTAAAGGTTTACAAGTATTTAGAAGTTTTTTCAGTTTCAGGCAAAATGTT  
ATGAAGTTTATTCCTCTTAAACATGGTTAGGAAGCTGTAGACGTTATTTGATTTTGTCTGGATT  
ATGTTTTCTGGAATAATTTTACCAAAACAGCTATTTGAGTTTTGACTTTCAGCAAGGCAAAACA  
TGACAGTGGATTCTCTTTACAAATGGAATAAAAAATCCTTATTTTGTATTAAGGACCTTCC  
TTTTTGTAACTAATCCTTTTTTATTGGTAAAAATGTAAATTAATATGTCAACTTG

**FIGURE 4**

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF  
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMLLMIP  
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL  
MFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL  
GDQ

**Transmembrane domain:**

amino acids 98-116, 152-172

**N-myristoylation site.**

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

**Glycosaminoglycan attachment site.**

amino acids 218-222

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**FIGURE 5**

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG  
 GTAGCTTCTATCCTGGGGGCTGAGCGACTCGGGGCCAGCTCTTCCCTACTCCCTCTCGGCT  
 CTTTGTGGCCCAAAGGCCTAACCGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTGCGC  
 CTTTGGGGCGGG**CAT**GGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG  
 CGGGGTTCCTGCGAGGCCAGACTGGTCCATCCCATCTTGACTTTGTGGAACAGAAATGT  
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT  
 GGCCTGTGTTCCCTTGTGTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC  
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGAATT  
 AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAGGC  
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA  
 AAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTACCT  
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT  
 GAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA  
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCAATTCAGTGAAGCTGCAATAATG  
 AATAATTTCCCAAGGGGATGGTGAACATTTTGCACACCCACCCTCAGAAGTTAAATGCATTT  
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGCTTGAAACTTCCTCCCTCC  
 CACAAAAAGGCCTGAAGATTCTTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC  
 TTATCAGTACTTGGAAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA  
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG  
 GAAAACCACTGGGGAGGTAGAGGAAATGACAGAGAAACCGAAATGACAGCAGAGGAGAGAG  
 CAAAACATTACTAAAGAGGAGATTGCTTGACAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**  
**A**TAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTTGTCTTAAAAATAAATTATTTAGTC  
 CTTACACTG

**FIGURE 6**

MAAEEDEVEWVVESIAGFLRGPDSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP  
LVFDDEEESKLTYTEIHQYKELVEKLLEGYLKEIGINEDQFQEACTIONPLAKTHTSQAILQP  
VLAADFTIFKAMMVQKNIEMLQAIRIIQERNGLPDCLTDGSDVVSDLEHEEMKILREVL  
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS  
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPANLSVLGTEELRQREHYLKQKRDKLMS  
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRLLAEKLKEEVINK

**N-glycosylation sites.**

amino acids 224-228, 246-250, 285-289

**N-myristoylation site.**

amino acids 273-279

**Amidation site.**

amino acids 252-256

**Cytosolic fatty-acid binding proteins.**

amino acids 78-108

**FIGURE 7**

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT  
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGTTACCTCAAAGAAATTGGAA  
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTTTGCAAAGACCCATACATCACAG  
GCCATTTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC  
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTA  
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT  
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

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**FIGURE 8**

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTG  
 TAGCTTCTCCACGTATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG  
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAAGCTCTTCTGAGGGAGGTAATTAACAAAC  
 AGTGGGA**ATG**GAAAAACAGTGGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC  
 ATTCTGCTAGGTGCCATATTTCATTGCTTTAAGCTCAAGTCCGATCTTACTAGTGAAGTATT  
 CTGCCAATGAAGAAAAACAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAAGTGT  
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAGTAG  
 AAATTTGAAATATGCTTCTCTGGAAGGAATTTCTGTGATTTCATGAAGTGGTCCATTCTGCCT  
 TTCTTTATTTCTCGGATAACTTGATTGTCTTCTATGTCTGTCTTATCTTCAACAGCCATG  
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGCTGAA  
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT  
 TGACTGCCGGGACTAAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTCATCACGATGCC  
 TTTTTCAGCCCTTCCAATTCCTGCCCTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAAATTG  
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTC  
 ACATCCGTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTTCTTCAATGGCT  
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCACTGAAAGCATGTTCTCATACA  
 GAACAGCAAATCTATTTCTTTGGCATTCTGTTTTAATGGGCTGACTCTGGGCTTCAGGAGA  
 GTAAACCGTGATCAGATTAGAAGCTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC  
 CTTATTTTTTGAAGTGCATTCCAGGGCCTTTTCAGTGGCTTTTCATTCTGAAGTTCTCGGATAA  
 CATGTTCCATGTCTTGATGGCCAGGTTACCAGTGTCTATTATCACACAGTGTCTGTCTGG  
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCATAGTCTCTCTCTATA  
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCCAAGAAGGATCCG  
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA  
 CCAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCT**TA**AGTGGTACCCACATAGTTTGCA  
 GCTCTCTGAACCTTATTTTACATTTTCAGTGTTTGTAAATATTATCTTTTCACTTTTGATA  
 AACCAGAAATGTTTTCTAAATCCTAATATCTTTGCATATATCTAGCTACTCCCTAAATGGTT  
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCTAAAGAAGTGATACAGGAGTAACA  
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT  
 TTTCTTGGCCTTCAAGCTTCCAAAAAACTTGTAATAATCATGTTAGCTATAGCTTGATAT  
 ACATACATAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT  
 CTCTCCCTTTTAAACATTATAAAAGCTAGGTTGTGCTTGAATTTTGGAGGCTTAGAGATAGT  
 CATTTTGAAGTAAAGAGACAACGGGACCCCTTCTAAAACGTTGGTTGAAGGACCTAAATAC  
 CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAAATATTTTGTCTGAAGAAGCAGT  
 TTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGGAAATTTGGATTTTTGT  
 AATAATCTTTGATGTTTTAAACATTGGTTCCCTAGTCAACATAGTTTACCACCTGTATTTTA  
 AGTCAATTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGGAGAGAAAAATCTTGAT  
 GTCATTACTCCTGAATTATTACATTTTGGAGAATAAGAGGGCATTTTTATTTATTAGTTACT  
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTCAGAACTACATC  
 CAGATTGTGCTGAGTGCATGCTAGGAACTTTAAAGGGATCCTTTCAAAGGATCACTT  
 AGCAACACATCTTGACTTTTAACTGATGATGAATATTAATCTCTAAAATAGAAAGACC  
 AGTAATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGTGATGGTATTTTTCATG  
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA  
 AAATTAGCAAAACAAAGTGACTTGTCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG  
 CTTTAAGTGGCAGGCTGTATGTTTACAGACTACCATCTGTAAGATGAGCTTTATGTGT  
 CATTTCTCAGAACTTTATACATTTTGTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA  
 AGGTAAATATACTATTATATAATTCATTGTGATATCCCAATAATATGACTGGCAAGAATTG  
 GTGAAATTTGAATTAATAATTTATAAACCT



**FIGURE 9**

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK  
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV  
 IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF  
 SPSNSCLLFRSECPKRDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI  
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI  
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI  
 YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESDETF

**Transmembrane domains:**

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,  
 298-318, 328-368

**N-glycosylation sites.**

amino acids 128-132, 204-208, 218-222, 374-378

**Glycosaminoglycan attachment site.**

amino acids 402-406

**N-myristoylation sites.**

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

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**FIGURE 10**

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG  
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC  
GTATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG  
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGGAATGGAA  
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG  
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG  
AAAACAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT  
TTCTGTGTGCTTGTGTCAATTCTGTGTTATAAAGAAAGATCATCAAGTAGAAATTTGAAATA  
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCCTGCCTTTCTTTATTTCC  
TGGATAACTTGATTGTCTTCTATGTCCTGTCTCTTCAACCAGCCATGGCTGTTATCTTC  
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGTAAGAGGCGCTAA  
CTGGATCCAGTGGGCTTCCTGCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA  
CTAAAACTTTA

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**FIGURE 11**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGCTAGCGCGCGGCGGCC  
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCCTGCGGGGCAGAGGAGCAT  
 CCCGCTACCAAGGTCCCAAGCGGCGTGGGCGCGGGTTCATGGCCAAAGGAGAAGGCGCGGAG  
 AGCGGGTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCGCGGCGCCA  
 GGTGAAGAAAGAACCCGAAAAAGAAACAAACAGTTGCTGTGTTGCAACAGCTTTGCTATG  
 CACTTGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC  
 CTATTGGATGTGGCTCAGGTGGGCCCTTTCTCTGCCCTCCATCATCCTGTTTGTGGGCGGAGC  
 CTGGGATGCCATCAGAGCCCCCTGTTGGGCTCTGCATCAGCAATCCCCCTGGACCTGCC  
 TGGGTCGCCTTATGCCCTGGATCATCTTCCACGCCCTGGCGCTCATTCGCCTACTTCCTC  
 ATCTGGTTCTGTCGCCGACTTCCACACGGCGGAGACCTATTGGTACCTGCTTTTCTATTGCCCT  
 CTTTGAACAATGGTCAGTGTTCATGTTCCTACTCGGCTCTCACCATGTTTCATCAGCA  
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGTGGGCAC  
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCTTGTTTCCAGG  
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACATGGCACCCTTCCACAG  
 AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG  
 TGCTGTCTCTGATCCTGGGCGTGGCGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG  
 AGCCAATCGCCTACTTCCGGGGCTACGGCTGGTCATGAGCCAGCGGCCATACATCAAATT  
 ATTACTGGCTTCCCTCTACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGT  
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT  
 CGGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT  
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA  
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCCTTCTTAC  
 TACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT  
 GGAACCGAGCCCATCTTCTTCTCTTCTATGTCTTCTTCCACCAAGTTTGCCCTCGGAGTGT  
 ACTGGGCATTCTACCCCTCAGTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC  
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATTGGCTCCCATAGTTCTCATCTG  
 CTGGGCCCTGCTGCTCTTCAAATGTACCCCATTTGATGAGGAGAGGCGGCGGAGAAATAGAA  
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG  
 AGCTGGCTAGCATCTCTAGGGGCCGCCACGTTGCCCGAAGCCACATGCAGAAGGCCACAG  
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA  
 CTGAAGACTCAAGAGGTTGGCCAGGACACTTGCTGTGCTCACTGTGGGCGCGGCTGCTCTG  
 TGGCCTCCTGCCTCCCTGTGCTGCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA  
 TGCCAAGGACTGATCGGGCTAGCCCGGAACACTAATGTAGAACCTTTTTTTACAGAGCC  
 TAATTAATACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGCTGTGAGCTA  
 TTAATGTTATTAATTTTCATAAAAGCTGGAAGC

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**FIGURE 12**

MWLRWALS LPPSSCLWAE PGMP SQTPWWAS ANPPGPAWVALCPGSSSPRPWPSLPTSSSG  
SCPTSH TARPIGT CFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL  
GTAIQQQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAV  
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPIYIKLITGFLFTSLAFMLVEGNFVLFACT  
YTLGFRNEFQNL LLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI  
ITYAVAVAAGISVAAAFLPWSMLPDVIDDFHLKQPHFHGT EPIFFS FYVFFTKFASGVSLG  
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL  
QALRDEASSSGCSETDSTELASIL

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**FIGURE 13**

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGCTGTATCTATATAATCTGT  
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA  
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA  
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT  
TGCACCTACACCTTGGGCTTCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC  
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG  
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC  
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT  
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG  
GAACCGAGCCCAT

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**FIGURE 14**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT  
 ATGAGCAGGTCTGAAGACTTAACATTTTGTGAAGTTGTAAAAACAGAAAACCTGTTAGAAATGT  
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT  
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT  
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG  
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCTGAA  
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG  
 ACTTTCATTTGTGGCAAACCTTCAGAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTG  
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG  
 CAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG  
 AGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTTGCACAGTGGCAATTTTGGGACTG  
 ATTTAGAACAGAACTCCATTGGAACCCGAGGACAAAGGTTATGTGCTTCACATGATCACT  
 ACTGCAGCAGAATGGTCTATGTCAATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA  
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG  
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTGATGAAGGAT  
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA  
 TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA  
 ATCAGGAAACATGAAGAAGCCATTTGATAGATTATTTCTAAAGGATATCATCAAGAAGACTA  
 TTAAAAACCTATGCTTATACCTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

**FIGURE 15**

MWWFQQGLSFLPSALVIWTSAAFIJSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI  
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG  
AVLTFMGSLYMFVQTIISYQMOPKIHGKQVFWIRLLVWCGVSALSMLTCSSVLHSGNFG  
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFSGFFLTYIRDFQKISLRVEANLHGLTYD  
TAPCPINNERTRLRSRDI

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**FIGURE 16**

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT  
TCCGTCTCTCGGGTCTTTTCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA  
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGGTGAAGCAGT  
TACCAAGAATCTTCAACCCTTTCCCAAAAAGCTAATTGAGTACAGTTCCTGTTGAGTACA  
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA  
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT  
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT  
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

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CCACGCGCTCCGCCCGCGCTGCGTCCCGGAGTGAAGTGAGCTTCTCGGCTGCCCGCGGG  
CCGGGGTGCAGGAGCCGACATGCGCCCGCTTCTCGGCCTCTTCTGGTCTTCGCCGGCTGCAC  
CTTCGCCTTGTACTTGTCTGTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG  
AGGCTGGAGGCAGGTGCTGTGGTTCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG  
GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCACGTGTTCTGCTCTTCTGCGGCGCCTA  
CCTCTACAAACAGGGCTTTGCCATCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT  
TGTTTGGCCATGGCTGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC  
TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTCTGATAAAGT  
GGCCTGCTGCAGAGAAAGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATTGTTTT  
TGAGACTTTTCCCATGACACAAACTGGTTCCTGAACCTCTCGGCCCAATTCTGAACATT  
CCCATCGTGAGTCTTCTCTCAGTCTTATCGGTTTGATCCCATATAATTTCATCTGTGT  
GCAGACAGGGTCCATCTGTCAACCTTAACCTCTCTGGATGCTCTTTTCTCTGGGACACTG  
TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCTCATTAATAAATTT  
AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA  
CACATGACTCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTGTGAATGGA  
TGTGGTCTCTAAAGCCCTCATTTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG  
CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT  
TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCCTCTAGAAAAATGCTGTTTGT  
GGCCGGGCGCGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC  
ACAAGGTCAAGGATTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT  
ACAAAAATTAGCCAGGCGTGGTGGCAGGCAGCTGTAATCCAGCTACTCGGAGGCTGAGGC  
AGGAGAATTGCTTGAACCAAGGTGGCAGGTTGCAGTAAGCCAAGATCACACCACTGCCT  
CCAGGCTGGGTGATAGAGTGAGACACTGTCTTGAC

**FIGURE 18**

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAE LRELSEVLREYR  
KEHQAYVFLFLFCGAYLYKQGFAPGSSFLNVLGALFGPWLGLLLCCVLTSGATCCYLLSS  
IFGKQLVVSYPDPKVALQRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPIVQFF  
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIK KFSQKHLQ  
LNETSTANHIHSRKDT

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 101-123, 189-211

**N-glycosylation sites.**

amino acids 172-176, 250-254

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 240-244, 261-265

**N-myristoylation site.**

amino acids 13-19, 104-110, 115-121, 204-210

**Amidation site.**

amino acids 27-31

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 4-15

**Protein splicing proteins.**

amino acids 25-31

**Sugar transport proteins.**

amino acids 162-172

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**FIGURE 19**

CCGAGGCGGGAGGAGCCCCGAGGGGGCGGAGCCCCGCATGAATCATTGTAGTCAATCATT  
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACGCCAGCTCAGAA  
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA  
 TTATGACAACTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG  
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACC  
 CCCCCGCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT  
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCCTTCT  
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA  
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGTGATGAAGACAGACCTTTTC  
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC  
 AACTGCAGTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCAAGGAA  
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATT  
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTGTAAGGGTTTTTCGCCAAG  
 TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA  
 CAGATCACAATGTTACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG  
 CCTCTTTAAACAAGTGCTCCTTTCTTACCACAGAACCTGTTGTGGGGAGTAAGATGCATAAG  
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA  
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG  
 ACACCAACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT  
 GGAACCGCTTTCTCAGAAGTGAGGAAATAGAACTGTGCACAGGAACAGCTTCAGAGCCGA  
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAA

**FIGURE 20**

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPYPLLIIVVY  
KVLATLGLILLTAYFVIQPFSPLAPEFVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL  
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT  
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFPYPWRRPLNRSQMLRELFV  
FTHLPFPKDasLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP  
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL

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**FIGURE 21**

CCACGGTGTCGGTTCTTCGCCCCGGCGGCAGCTGTCCCGAGGCGGGAGGAGCCCGAGGGGCG  
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTCCAGTTCTCAGCCGTTTCAGTTGTGATC  
AAGGGACACGTGGTTTCCGAACGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT  
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTTCAGAGACTGTTG  
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTGAGAGAAGGCAATTGAAAAATTTATC  
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT  
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC  
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

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**FIGURE 22**

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG  
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGGTGGTG  
 CCACTGGTGGCAGCGCTCTAGACCGTGCTATGAGCGCTGGGGCTGCAGTGGGGACTGCC  
 CTCCCTTGGCACCACCAATTGGCAGCCCCACTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA  
 CACCCGAATTGGCGCCACTTTCATCGACAAACAGGTACAGCCAACTTCCAGTTCGAAATG  
 GACACCTATGTCTAAGAGCCAGCACTTATGTAGGTTTCTGGAATGCCCTGTATGACATGTT  
 TATGACAGTGGGAGCGCGCCAGTGGGAGCGCGCCAGAGTCGTGGGGCTTCCAGGAGC  
 TGTGCTTGGAACTTGGCAGAGGCGGGCGCGCTGGAGGGCTACGCTACACGGCAGTGCTG  
 AAGCAGCAGCAACGCAGCACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGT  
 CGCCAGCCATGTGGGGCTGGGGCTGAGGGACACTCCCATCCCCCGCTGGAACACTGTCCA  
 GCGCCGAGACATATTCACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCTCAC  
 CTGGAACTCAGCGCTCTCCGAGACAACTCTGGGTGAGGTTCCCTTGACACCACCGAGGAGGC  
 CTCACCTGCCCTTGCAGTGAACCAAGAGGCCAAAGTGAGCAGCCCAACCCAGTGTGCTGCAGG  
 AGGACAGCTCGGGCAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCGAGCAACTG  
 GATGACAGCGCTGAGAAGCTGGTCTGTGGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT  
 GGTCCAGGGCTGTGGAGGTCAACACAGAATGTATACTTCTACGATGGCAGCACTGAGC  
 GCTGGAACACCGAGGAGGCGCATCGGTATGATTTCCGGCGCCCATGCCCGAGCTGCGTGAG  
 GTCCACTTGGCGCTTCAACCTGGCGCTTCAAGCACTTGAAGCTTCTTTATCGATCAGGC  
 CAACTACTTCTCAACTTCCATGCAAGGTGGGCAGCAGCCAGCTCATCTTATCGCAGCA  
 CTCGAGACCCAGCTGGCCCCATCCACCCCATACCCAGGTACGGGAACCGAGGTGTACTCG  
 TGCTCTTGGCGCTACGGCCCTTCAAGGCTACCTAAGCAGCGCTCCCCAGGAGATG  
 GCTGGCTGGCTCAGGCCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACTTCGAGTACT  
 TGTGCAACTCAACACCATTTGCGGGCGGAGCTACAATGACCTGTCTGAGTGGCTGTGTTG  
 CCTGGGTCTGTGAGGACTACGTGTCCCCAACCTGGACCTCAGCAACCCAGCGCTTCTCCG  
 GGACCTGTCTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAGAATG  
 ATGAAAGCTTTGAGGACCCAGCAGGGACCAATTGACAAGTTCCACTATGGCAACCCCACTCTCC  
 AATGACGAGCGGCTATGCACTACCTCATCGCGTGGAGCCCTTCACTCCCTGCAGTCCA  
 GCTGCAAGAGTGGCGCTTTGACTGCTCCGACCGGCAAGTTCCACTCGGTGGCGGAGCGCTGGC  
 AGGCACGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGAATTCTTACTTTCCCT  
 GACTTCTTGGAGAACCGAAGCGGTTTGAACCTGGGCTGTCTCCAGCTGACCAACGAGAAAGT  
 AGCGATGTGGTGTCTACCCCTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCCGC  
 AGGCTCTGGAGTCCGAGTATGTGTCTGCACCTACACGAGTGGATCGACCTCATCTTTGGC  
 TACAAGCAGCGGGGCGAGCGCGCAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA  
 GGGGGCTGTAGACTTGGACATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTGA  
 TCAGCAACTTTGGGCAGACTCCTGTGACGTGCTGAAGGAGCACATCCAATCGGCTCTCA  
 GCTGGAGGAAGCAGCCCATCGCTTGCACGCTGGACACTAATCACTAGCATCTTCCAGCA  
 CCTGGAGCAACTCAAGGCATTTCTCGCAGAGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA  
 CCCACAGCTGGTTGGCTATGACCGCAACATAAGCACTACTTCAGCTTCAGCAAAAGACCCC  
 ACCATGGGCGGCCAAGAGCAGCGACTGCTGAGTGGCCGCTGGGTGCCAGGCGAGTGGTGT  
 GAGTGGAGCAAGCACTGGCAGTGGCCCCGATGGAAGCTGCTATTACGCGGTGGCCACTGGG  
 ATGGACGCTTGGGCTGCTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC  
 CTTGATGTAGTAACCTGCCCTGCACTGGACACTGTGGCATCTACCTCATCTCAGGCTTCCCG  
 GGCACACCACTGATGGTGTGGCGGCTCCTGCATCAGGTGGTCTGTGCTAGGCGCTGGCAG  
 CAAAGCTGTGCAAGTCTGTATGGGCAATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT  
 GAACCTGACATGGCTGTGTCTGATCTGAGGATGGAACCTGTGATACACACTGTACGCGC  
 CGGACAGTTTGTAGGCGCACTACGGCTCTGGGTGCCACATTCCTTGGACCTATTTTCCACC  
 TGGCATTTGGGTGCGGAAGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACCTCTGGGGCC  
 CAGGTCACTACTCTTGCACCTGTATTCAGTCAATGGGAAGTTGCGGGCTTCACTGCCCT  
 GGCAGAGCAGCTCAGCCCTGACCGGTGACAGAGGACTTTGTGTTGCTGGGACCGCCAGCT  
 GCGCCCTGCACATCTCCAACATAACACACTGCTCCCGCGCCGCGCTCCTTGGCCATGAAG  
 GTGGCCATCCGACCGGTGGCGGTGACCAAGGAGCGCAGCCAGCTGCTGGTGGGCTGGAGGA  
 TTGGCAAGCTCATCTGTTGGTGGTGGCGGGGACGCCCTGTAGGTTGGCAGCAGCGAGTTCGCGC  
 GGAAGCTGTGGCGGTGCTCGCGCGCATCTCCACGGTGTCTCGGAGAGCAGGAATAACAAC  
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGCTGCTCGGGCCCCCGCCCCGCGAGCGCTG  
 GCGCGGAGGCCCGCCAGAAGTCCGCGGGGAACCCCGGGTGGGACGCCAGGCGGTGA  
 GCGGGGCCACCTGCCAGCTCAGGATTGGCGGGCATGTTACCCCTCAGGGATTGGCG  
 GCGGGAAGTCCCGCGCTGCGCGCTGAGGGCGCGCTGAGGGCCAGCATGGCGCT

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**FIGURE 23**

MSQFEMDTYAKSHDLMSSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL  
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVN  
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALET  
 MEAAELDEQREKLVLSAECQLVTVVAVVPGILLEVTQNVYFYDGGSTERVETEEGIGYDFRRP  
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPQTTPRPQPGPIPHPTQV  
 RNQVYSWLLRLRPPSQGYLSSRSPEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL  
 SQYPVFPWVLQDYVSPITLDSLNFPAVFRDLSPKIGVVNPKHAQLVREKYESFEDPAGTIDKFL  
 YGTHYSNAAGVMHYLIRVEFFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADVKEIP  
 EFFYFPDFLENQNGFDLGLCLTNEKVGDDVLPWPASSPEDFIQHRQALESEYVSAHLHEW  
 IDLIFGYKQRGPAEEALNVFYCYTEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP  
 HPTRLSAEEAAHRLARLDTNSPISIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF  
 SFSKDPMTGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL  
 SQLSCHLDVVTCALALDTCGIYILISGSRDTCMVWRLRHQGGLSVGLAPKPVQVLYGHGAAS  
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGOIVVQSSA  
 WERPGAQVITYSLHLYSVNGKLRLASPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA  
 PPLPMKVAIRSVAVTKERSHVLVGLDGLKLVVVAGQPSEVRSSQFARKLWRRSSRRISQVSS  
 GETEYNPTAR

**N-glycosylation site.**

amino acids 677-681

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 985-989

**Tyrosine kinase phosphorylation site.**

amino acids 56-65, 367-376, 543-551

**N-myristoylation site.**

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,  
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,  
 873-879, 912-918, 954-960

**FIGURE 24**

CGGACGCGTGGGCGGACGCTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC  
 CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT  
 CCAAAGGCCAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTTGGGGCTCTTC  
 TGGACCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCTCTGCTGGAGCCTTTGCCTCCTT  
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC  
 GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG  
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC  
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAATAATTTATCAAGTTC  
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA  
 AATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGTCTGCTGGACAAAGTACAGA  
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTGGAGGCGTGGGGTCTGTCTTCTTTT  
 TTTTCTCCGGTCGCATCCCGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC  
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTACGCGT  
 TTTCGGCATGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG  
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC  
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCTCCGGCCCTGATCCAGGACTGC  
 ACCCCACCCCAACCGTCCAGCCATCCAACCTCACTTCGCCCTTACAGGTCTCCATTTTGTGGT  
 AAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCAGCCTGTAATCCAACACTTTGAGAGGCTG  
 AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAACCTCC  
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC  
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA  
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA  
 AAGATTTTATTAAAGATATTTGTTAATC



**FIGURE 25**

RTRGRTRGGCEKVPINTSCNPHTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLE  
WTLNWWLALGQCVLAGAFASYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ  
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK  
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGVGVLSTFFFSGRIPGLGKDFKSPHLNYY  
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMKSLLKILGKKN  
EAPPDNKKRKK

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**FIGURE 26**

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGCGCCCGCT  
 GGCT**ATG**TTTCGTGTCCGATTTCCGCCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC  
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCCTCAGGCCTTGTGTC  
 CAGTGTGACACAGTGAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAAGCTGAAACTGC  
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG  
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG  
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAACAAGATGA  
 TGACCTTGAAGTTCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT  
 CAGGAAATGACAGTGATGGGTGACAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA  
 GTGGAGCAAACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCGAGAAGAGACATCCT  
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG  
 CTTGGATGCTGTCCAAGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC  
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG  
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA  
 CACGGATCTCCTTTGAGTATGACCTCCGCCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC  
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA  
 GCGGCTCCAGGAGTTCCTTGCCAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC  
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAATAAA  
 TTTGGGATGAAGGACATGCGCTGCAGACTTTCAGCATTTTGGGTTCAAGCACAAAGTT  
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT  
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG  
 TACCATGGCTGGAACCTGCACAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTTGCCAGCTGC  
 CTTTGACCAACCTCGTCATCTCCAGGGGCTTTTCTGTACTGCTCTCTCATGGAGGGCAC  
 TCCAGATGTGATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA  
 AGTCTTTGTGTGTTTCGACAAAGAACCGGCTGCAAACTGCTGCCCTGGTGATGGCTGCC  
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC  
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAAGGCAGCGGAAAGCACCAGCTCCCGGA  
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT  
 CTGGACGCACTTATTTCCCTCCTGTCT**TAG**GAATTTGATTCTCCAGAATGACCTTCTTATT  
 TATGTAAGTGGCTTTCATTTAGATTGTAAGTTATGGACATGATTGAGATGTAGAAGCCATT  
 TTTTATTAATAAAATGCTTATTTTAGGAAA

**FIGURE 27**

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF  
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD  
LEVPAYEDIFRDEEEDDEHSGNDSGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF  
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWVAIVGLTDQWVQDKITQMKYVTDVGVLQRH  
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKR  
LQEFLLADMGLPLKQVKQKFQAMDISLKENLREMIIESANKFGMKDMRVQTFSIHFGFKHKFL  
ASDVVFATMSLMESPEKDGSGTDHFTQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL  
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP  
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL  
DALISLLS

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**FIGURE 28**

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCGTGGCTATGNTCGTGTCCGATTTCCGCA  
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT  
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT  
GGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC  
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT  
GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA  
CGATACCC

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**FIGURE 29**

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTCCAGTACCATTTTTTCTAGTGAAC  
 CACGAAGGGACGATACCGAGAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCAATTG  
 GCTGACTTTTGGCTATAGAAAAAGAAAGGAACGAAAAGAGACACTTTTTTTTGGAAAGCTAA  
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAATT  
 GAGTAAAGTACGCTCCGGTCAACC**ATGGT**GACAGCCGCCCTGGTCCCGCTTGGGCAGCGCTC  
 CTGCTCTTCTTCCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC  
 CAGCGGCTGACCAACGGTGTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAG  
 CCTCTTCTCTCCGGCCGCCACGCCCTGCTGAGATCAGACCTTACATTAATATCACCATC  
 CTGAAGGGTGACAAAGGGGACCCAGGCCAATGGGCTGCCAGGGTACATGGGCAGGGAGGG  
 TCCCCAAGGGGAGCTTGGCCCTCAGGGCAGCAAGGGTGACAAAGGGGAGATGGGCAGCCCCG  
 GCGCCCGTGCCAGAAGCGCTTCTTCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC  
 GCGCAGGACTTCCAGACGCTGCTCTTGAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA  
 CATGGCCACGGGCAGTTTGTCTGCTCCCTGCTGGCATCTACTTCTTACGCTCAATGTGC  
 ACAGCTGGAATTACAGGAGACGTACGTGCACATTATGCATAACAGAAAGAGGCTGTCATC  
 CTGTACGCGCAGCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC  
 CTACGGGACCGCTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCA  
 ACGACTTCGACACCTACATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGAC**TG**AGGG  
 CCTCTGGGCCACCTTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGCTCCCTGCAGGGCTCAG  
 TTGCACTGCTGTGGAAGGCAAGGCCAGGAGGTCCCGGGGACCTGGCATCTTGGGGAGA  
 CCTGCTCTTATCTTGGCTGGCATCATCCTCCAGCCTATTTCTGCTCTCTCTCTCTCTCT  
 TGGACCTATTTTAAAGAAGCTTGCTAACCTAAATTTCTAGAACTTTCCAGACCTCGTAGCCC  
 AGCACTTCTCAAATTTGGAAATGCATGCAATACCCCGGGTTCGTGTTAAATGCAGATTCT  
 GACTCAGCAGGCTTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTGGGTGATGCTG  
 ATGGGGTTCAGTCTATGAACCACTGGAGCAACAGGTTCTAGGACTTTCTCAATATTCTAG  
 TACTTCTGAACATTCTTGAATCTTCCCACATCTAGAATTCTCCAACATTTTTTTTTTCT  
 TGAGACAGAGTCTTGCTCTGTTGCCCAGGCTAGAGTGCAAGTGGTGCATCTCAGTTCACTGC  
 AACCTCTGCCCTCCCGGGTTCAAGCGATTCTTCTGCTCAGCCTCCCTAGTGGCTGGGATTAC  
 AGGCTCCTGCTTACCATGCTGGCTAAATTTTGTATTTTGTAGTAGAGATGGGGTTTACCATA  
 TTGGCCAGGCTGGTCTTGAACCTCTGACTTCAGGTGACCCACCCCTCGGCCCTCAAAAAT  
 CCTGGGATTCAGGTTGTAGCCACCGTGCTGGCCCAATTCCAACATTCTTAAATTTCTCTCAT  
 CCTCCAGGGCTCCCGTGCTATGTTCTTTTACCCCTTCCCGCTCTTCTCTTGTCTCAGGCC  
 TGCAACCTGCAAGCCACCGTTCAATTTATTATTATTAACACTGAGCACTCAGTCTGTGCT  
 GGGTCCCGGGAAGGGTGAGGGGGTCAAGACAGGCCCCGCCCCCTGAGTCTGGCTGACTGGCCA  
 GTCCAGCCCAAGCGGGGAGAGATGTGTACATAGGTTTAAAGCAGACCCAGAGCTGTGGGG  
 GCTGTGTTCTGGGTGTTTCAAGTGCTGCTGGTCTTCCATTACCCACTGCTCCCCAAGGCTGG  
 TGGGACGGGGTCCCGGTGGCAGGGGAGGTATCTCTTCCCGTTCTCATCCACCTGCCCCAG  
 TGCTCATCGTTACAGCAAACCCAGGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG  
 ACCCAGGATGTGGGGGCTATTGGGGGGTGAAGTGGCCCCGGAAGATGGAACCCACACCCA  
 TAGCTCTCCCCACAGCTGATAGGCCATCTTGCAGAGAAGCTGCCCTCCTCAGTGGGATCCC  
 CTTCCTGCTCTCTCCAGGGGCTCTGCCAGGGGCTTGCTCAGTCCCTTCCACCAAGTCACT  
 GAACCTCCGTTTCCCAAGGCTCCAGGCTGCCCTCAGACACTGATGTCTGTCCGTCAGGTGCT  
 CTCTGCCCCCTCATGCCCCCTCACCGGCCAGTCCCCGACTCTCAGGCTTTATCAAGGTG  
 CTAAGCCCCGGGTGGGCACTCTCGTCTCAGAGCCCTCTCCGGCTGGTGTGCTCTTTAC  
 AAACACTGCAAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCTCAGCAGGTCTGGGG  
 AGCTAGAGCAAAGGAGGACCTCAGGCTTCCGTTTCTCTTCCAGGGTGGGGTGGCTGGT  
 GTTCCCCTAGCTTCCAACCCAGGTGGCTGCCCTTCTCCCCAGAGGGAGGGCGGCTCCGC  
 CCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGTGATCTCTCTGGTGCTCAC  
 AGGCCAGGGGAGCCGTGGCTCCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGCCAGGA  
 AGACCTGTGCTATAAACACCCTGCCTGATCCTGCCCTGCCCTGACCCGCCACGCCCTGCC  
 GTCCAGCATGATTAAAGAATGCTGCTCTCTTGGAAAAAAGAAAAA

**FIGURE 30**

MVTAALGPVWAALLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH  
ALPEIRPYINITILKGDKGDPGMPGLPGYMGREGPQGEPPGQGSKGDKGEMGSPGAPCQKRF  
FAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET  
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT  
FSGHLIKAEDD

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 72-75

**Clq domain proteins.**

amino acids 144-178, 78-111 and 84-117

**FIGURE 31**

ACTCGAAGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCGACCCGCCAGGAAAGACTG  
 AGGCCGCGGGCTGCCCGCGCCGGCTCCCTGCGCGCGCGCGCTCCCGGGACAGAAAGATG  
 CTCACAGGGTCCCTGCTGCTGCCGTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG  
 GCTGGCCATCGGGTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCAGTGGCCGCCAGGGG  
 ACCACGGTGCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAAGGGCAT  
 CACCATGCTGCAGCAGGACAGCTTTGCCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTAC  
 AGAACCAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTG  
 GACCTGACGGCCAACAGGCTGCATGAAATCACCATGAGACCTTCGTGGCCTGCGGCGCT  
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC  
 TCGACCGCTCTGGAGCTCAAGCTGCAGGACACAGAGCTGCGGGCACTGCCCGCGTGC  
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGCAT  
 CCTGGCACTGCCAACCTGGAGGCGCTGCGGCTGGCTGGGTGCGAGAGCTGGACG  
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG  
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACGCGCTCGGGTGGCCGGCAACAC  
 CCGCATTTGCCAGCTGCGGCGCAGGACCTGCGCGGCTGGCTGCCCTGAGGAGCTGGATG  
 TGAGCAACCTAAGCTGCAAGGCTGCTGCTGGCGACTCTCGGGCTCTTCCCGCGCTGCGG  
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTTGAAGCTGGTTCGGCCCTG  
 GTTGGCGGAGGACAGCTCAGCTGCGGACGCTTGAGGAGACGCGCTGCCACTTCCCGCCCA  
 AGAAGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCGGACTTTGGCTGCCCGCCACACAC  
 ACCACAGCCACAGTGCCCAACACGAGGCGGCTGGTGCAGGAGCTTGCCTTCTCTAG  
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCGGCCACTGAGGCCCCAGCCCGCTTCCA  
 CTGCCCCACCGACTGTAGGGCTGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCT  
 AATGGGGGCACATGCCACCTGGGGACACGGCACCCTGGCGTGTGTGCCCCGAAGGCTT  
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA  
 CGCCGAGGCCACACCGTCCCTGACCTGGGCATCGAGCGGTGAGCCCACTTCCCTGCGC  
 GTGGGGCTGCAGCGTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCTCCGTCTCACCTA  
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG  
 AGTACACGGTCAACAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGG  
 CCGGGCGGGTGCCGGAGGGCGAGGAGGCTGCGGGGAGGCCATACACCCACAGCCGTCCA  
 CTCCAACACGCCCGAGTCAACCAAGGCCGCGAGGGCAACCTGCCGCTCTCATTTGCCCGG  
 CCTGGCCCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACAGCTACTGTGTGCGGGG  
 GGGCGGGCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCC  
 TGGAACTGGAGGGAGTGAAGTCCCTTGGAGCCAGGCCGGAACAGAGGGCGGTGGAG  
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCTGGCCTC  
 CAGTCAACCTCCAGCAGAAAGCCTACATCTAGGCCAGAGAGAGAGAGGCGAGCTGGGGCCG  
 GGCTCTCAGCGAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACACGTAAGTTCTCAGTCC  
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGGCTGTTCCTCTGGA  
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCGAGCTGACGAGCCCTAACGTCCCCAGAAC  
 CGAGTGCCATGAGGACAGTGTGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGACGGCG  
 GGCCCTGCCATGTGTGTTAACGCATGCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA  
 CCTTGGGGGCTGAGGAAGCTCCCGAAAGAGCAGAGGAGAGCGGGTAGCGGCTGTG  
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAGGAAGATGCTTTA  
 GGAACATGTTTTGCTTTTTTAAATATATATTTATAAGAGATCCTTTCCCATTTATTTCTG  
 GGAAGATGTTTTTAAACTCAGAGACAAGGACTTTGGTTTTTGAAGACAACGATGATAG  
 AAGGCCTTTTGTAAGAAAAATAAAAGATGAAGTGTGAA

**FIGURE 32**

MCSRVP L L L L L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P D T V G L Y V F E N  
G I T M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R  
R L E R L Y L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P I R L P R L L L L D L S H N S L L A L E P  
G I L D T A N V E A L R L A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G  
N T R I A Q L R P E D L A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G  
P W V R E S H V T L A S P E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S  
S S L A P T W L S P T A P A T E A P S P P S T A P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E  
G F T G L Y C E S Q M G Q T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L  
T Y R N L S G P D K R L V T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A  
V H S N H A P V T Q A R E G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R R G R A M A A A A Q D K G Q V G P G A G  
P L E L E G V K V P L E P G P K A T E G G E A L P S G S E C E V P L M G F P G P L Q S P L H A K P Y I

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**FIGURE 33**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGC AAGCCGTGGGGGTTTTGAGCTCAT  
 CTTTCATCATTCATATGAGGAATAAGTGGTAAAAATCCTTGGAAAAATCAATGAGACTCATCAG  
 AAACATTACATATTTTGTAGTATTGTTATGACAGCAGAGGTGATGCTCCAGAGCTGCCAG  
 AAGAAAGGGAACCTGATGACCAACTGCTCCAACTGTCTCTAAGAAGGTTCCCGCAGACTTG  
 ACCCCAGCCACAAACGACACTGGATTATCCTATAACCTCCTTTTCACTCCAGAGTTCA  
 GTTTTCATTTCTGCTCCAAACTGAGAGTTTGTATTCTATGCCATAACAGAAATCAACAGCTGG  
 TCTCTAAAACCTTTGAATTCACAAAGGAGTTAAGATATTAGATTGTCTAAATAACAGACTG  
 AAGAGTGTAACTTTGGTATTTTACTGGCAGGTCTCAGGTATTAGATCTTTCTTTTAATGACTT  
 TGACACCATGCTTCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA  
 GTGGGGCAAAAATACAAAATCAGATTCCAGAAAAATTGCTCATCTGCATCTAAATACTGTCT  
 TTCTTAGATTTCAGAACTCTTCTCATTATGAAGAAGTAGCTGCCCATCTTAAACACAAC  
 AAAACTGCACATTGTTTTACCAATGGACAAAAATTTCTGGGTTCTTTTGGCTGATGGAATCA  
 AGACTCAAAAATATTAGAAATGACAAAATATAGATGGCAAAAGCCAATTTGTAAAGTTATGAA  
 ATGCAACGAAATCTTAGTTTAGAAAAATGCTAAGACATCGGTTCTATTTGCTTAATAAAGTTGA  
 TTTACTCTGGACGACCTTTTCTTATCTTACAATTTGTTGGGCATACATCAGTGGAACT  
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC  
 TCAAAATCTGTAATGAGAACTATAAAATGGAGCATGTACATTTACAGAGTGTTTTACATTCA  
 ACAGGATGAAATCTATTGTCTTTTGACCAAAATGGACATAGAAAATCTGACAAATCAAAATG  
 CACAAATGCCACACATGCTTTTCCCGAATTCCTACGAAATTCGAATTTTAAATTTTGGC  
 AATAATATCTTTAACAGACGAGTTGTTTAAAAGAACTATCCAATCGCTCACTTGAAAATCT  
 CATTTTGAATGGCAATAAATGGAGACACTTTCTTTAGTAAGTTGCTTTGTCTAACACACAC  
 CCTTGGAACTCTGGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA  
 TGCCCAAGAACTGGGTCAATATGAATCTGTCTACAATAAATTTGCTGATTTCTGTTCTCAG  
 GTCTTGGCCAAAAGTATTCAAATACTTGACCTAAATATAAACCAAAATCAAACTGTACCTTA  
 AAGAGACTATTATCTCTGATGGCCTTACGAGAAGTAAATATTGCAATTTAAATTTTCTAAGTAT  
 CTCCTTGGATGCTGATCATTTCAGTAGACTTTCAGTTCTGAACATTGAAATGAACTTCTATTCT  
 CAGCCCATCTGCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACCTCTAAATGCGGGAAGAA  
 ATCCATTCGCGTGTACCTGTGGAATAAAAAATTTCAATCAGCTTGAAACATATTCAGAGGTC  
 ATGATGGTTGGATGCTCAGATTATACACCTGTGAATACCCCTTTAAACCTAAGGGGAACATG  
 GTTAAAAGACCTTCTATCTCCACGAATTTATCTGCAACACAGCTCTGTTGATTTGCACCAATG  
 TGGTTATTATGCTAGTTTCTGGGGTTGGCTGTGGCCTTTCTGCTGCCACTTTGATCTGCC  
 TGGTATTCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGTTAGGAAAACAAACCCA  
 AGAAACACTCAAGAGAAATGTCGGATTCCACGCATTTATTTTATACAGAGTGAACATGATTTCT  
 GTTGGGTGAAGAAATGAATGATCCCCAATAGAGAAGGAAGATGGTTCTATCTGATTTGCT  
 CTTTATGAAAGCTACTTTGACCTGGCAAAAGCATTAGTGAATAATTTGAAGCTTCAATTGA  
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT  
 ATGAATTTCTACTTTGGCCACCACAATCTCTTCCATGAAAATCTGTATCATATAATTTCTATC  
 TTACTGGAACCCATTCATTTCTATGCAATTTCCACAGGATCATATAACTGAAAGCTCTCCT  
 TGAATAAAAGCATACTTTGGAATGGCCCAAGGATAGGCGTAAGTTGGGCTTTTCTGGGGCA  
 ACCTTTCAGCTGCTATTATGTTAATGTTATGATAGCCACAGAGAATGTTGTAATGCTCGAGCA  
 TTTACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGTATGAGACAGATTGTCT  
 ATAAAATCCCACAGTCCCTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTGATA  
 CAACCTTTATGATGGCAATTTGACAAATTTTATTAATAAATAAAATGGTTATTCCCTTCATA  
 TCACTTTCTAGAAGGATTCTAAGAATGATCCTATAGAAAACACCTTCAAGTTTATAAAG  
 GTTTATGGAATAAGGTGTTCTATCCAGGATTTGTTTAAATCATGAAAATGTGGCCAGGTGCG  
 AGTGGCTCAGCTCTGTAATCCCAGCACTATGGGAGGCAAGGTGGGTGAGCCACAGGAGTCAA  
 GAGATGGAGACCATCTGCGCCACATGGTGAACCCCTGTCTCTACTAAAAATACAAAATGCTA  
 GCTGGGCGTGATGGTGCAAGCCTGTAGTCCAGCTACTTTGGGAGGCTGAGGCGAGGAGTACG  
 CTTGAACCCGGGAGGTGGCAGTTGCAATGAGCTGAGATCGAGCCATGCACTCGAGCTGGT  
 GACAGACCGGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGGAACATCCT  
 TCAATGGCCACAAAAATGAAGTCTAATTCATTAATATATAGTACATTAATGTAAATATATATTA  
 CATGCCACTAAAAAGAAATAGGTAGCTGTATATTTCTGGTATGAAAAAATATTAATATAT  
 GTTATAAACTATTAGGTTGGTGCAAACTAATTTGGTGTGTTGTCATGAAATGGCATTTGAA  
 ATAAAAGTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGTCTGGGAGGTGGA  
 TTACAGGAGCAATTTGATTTCTATGTTGTATTTCTATAATGTTTGAATTTGTTAAGATGA  
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

**FIGURE 34**

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ  
LQSSDFHVSVKLRVLILCHNRIQQLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL  
SFNDFDTPICEEAGNMHLEILGLSGAKIQKSDQFKIAHLHLNTVFLGFRTLPHYEEGSLP  
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL  
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR  
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNfANNILtDELfKRTIQLP  
HLKTLILNGNKLEtLSLVSCFANNTPLEHLdLSQnLLQhKNdENCsWPETvVNMNLSYNKLS  
DSVFRCLPKSIQILDlnnnQIQtVPKETIHLmALRElNIAFNfLTDLPGCSHfSRlSVLNIE  
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNfIQLEtYSEVMMVGWSDSYTCEYPLN  
LRGTRLKDVHLHELSCNTALLIVtIVVIMLVGLAVfCCLHFDLPWYLRMLGQCTQTWHRV  
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYfDPGKSISENI  
VSfIEKSYKSIfVLSPNFVQNEWCHYEFYfAHHNLfHENSdHIILILLEPIPFYCIPTRYHK  
LKALLEKKAYLEWPKDRRKCGLEFWANLRAAINVNLATREMYELQTfTELNEESRGSTISLM  
RTDCL

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[illegible]

**FIGURE 36**

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPPYARPEPELETFSPLP  
AGPGEWEWRRPQEP RPPK RATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS  
VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRRLNIQAGINENDFYDGAWCA  
GRNDLQQWIEVDARRLRTFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNKSGDMIF  
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNYYHRRNEMTT  
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF  
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG  
SELGGWSLGRWTHDGDIDNNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA  
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYST  
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGC DKYPHES  
QLPEEWENNRESLIVFMEQVHRGIKGLVRD SHGKIPNAIISVEGINHDIRTANDGDYWRLL  
NPGEYVVTAKAEGFTASTKNCMVG YDMGATRCDFTL SKTNMARI REIMEKFGKQPVSLPARR  
LKLGRKRRRQRG

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**FIGURE 37**

CTAAGAGGACAAGATGAGGCCCCGGCTCTCATTCTCTAGCCCTTCTGTTCTCTTGGCCAAAGCTGCAGGGG  
 ATTTCGGGGGATGTGGGACCTCCAATTCCAGCCCCGGCTTCAGCTCTTCCAGAGTGTGACTCCAGCTCCAGC  
 TTCAGCTCCAGCTCCAGGTGGGGTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTTCTGTGTCTCCAGTGTGT  
 TTCCAATTTCCACGGCTCCGTGGATGACCTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACACCTTTTC  
 CCGTGGACAGAGTGAAGCCTTGGAAATTCACAGCTCATGTTCTTCTCAGAAGTTTGAGAAAGAACTTTCTAAA  
 GTGAGGGGAATATGTCCATTAATAGTGTGTATGAAAAGAACTGTTTAAACCTAACTGTCGGAATTGACATCAT  
 GGAGAAAGGATACCTTTTCTTACACTGAAGTGGACTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC  
 TGCTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATTTGTACACAGCTGGAGGTGGAGATAAGAAAT  
 ATGACTCTCTTGGTAGAGAGCTTGAGACATAGACAAAAAATGTCCTTGCCATTGCCGAGAAATCTGTGGC  
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTTAAAGATCAAAACACCCCTTGTGCTCCGAGAAATCTGTGGC  
 CAGGGAGCTGTGTGTGTGTGTGTGGAACATCAGCAACCGCTGTGTGGTTCAGCTCAACTGGAGAGGGTTT  
 TCTTATCTATATGTGCTTGGGGTAGGGATTACTCTCCCGAGCATCCAACAAAGGACTGATTTGGGTGGGGCC  
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTGTCTATTGTATATAA  
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAAGTAGTGGTACAGCAGTTTACAACAACACATGTAGTCAAC  
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTGACCACCAACAGATTTGCTGTGACTCAAATCTCCCTAA  
 TGCTGCCATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG  
 GATTTGGGTTATTTATCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACTCT  
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCAACGCCCTTCATGGTATGTGGGGTTCT  
 GTATGCCACCGCTACTATGAACACCAGAACAGAGAGATTTTTTACTATTATGACACAACACAGGGAAAGAGG  
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTGACCAGAAA  
 CTTTATGTCTATAACGATGGTTACCTTCTGAATTATGATCTTCTGTCTTGCAAGAGCCCGAGTAAAGCTGTTTA  
 GGAGTTAGGGTGAAGAGAAAAATGTTGTGTGAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT  
 CTGAAAAGTGTGTTCTTTTGCAGCAATGTTTAGGTGCATAGTTTACCACACTAGAGATCTAGGACATTTGTCT  
 TGATTTGGTGAGTTCTTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGCAATAAAGTGTGCTAGGGTGGGA  
 TTGTCAAGAGTCTAGGGCCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCTTAAATTA  
 GGAATTAAGGACTTAAACTCAGTATGGCTCTAGGGATTCTTTGTACAGGAAATATTGCCCAATGACTAGTC  
 CTCATCCATCTAGCACCACTAATTTCTTCATGCTGGAAGAAACCTGGGAGCTTAGTTAGGTAGATTAATATCT  
 GGAGCTCTCGAGGGACCAAACTCTCAACTTTTTTTCCCTCACTAGCAGCTGGAATGATGCTTTGTATGTGG  
 CAGATAAGTAAMTTGGCATGCTTATATATTCTACATCTGTAAGTGCTGAGTTTTATGGAGAGAGGCCCTTTT  
 ATGCATTAATTTGTACATGGCAATAAATCCAGAAGGATCTGAGATGAGGCACTGCTTTTCTTTTCTCTC  
 ATTGTCACCTTACTAAAGTCAGTAGAATCTTACCTCATAACTTCTTCCAAAGGAGCTCAGAAGATTAG  
 AACAGACTTACTAACCAATTCACCCOCCACCAACCCCTTCTACTGCTACTTTAAAAAAATTAATAGTTTT  
 CTATGGAACTGATCAAGATAGAAAAATTAATTTCTTAAATTCATTATGAGACTTTTATTTACATGACTCTA  
 AGACTATAAGAAATCTGATGGCAGTGACAAAGTGTAGCAATTTATTTGATATAAAGACCTTGGAGCATA  
 TGTGCAACTTATGAGTGTACAGTTTGTGCATGTAATTTTGCCTTGTGTTAAGCCTGGAACCTGTGAAGAAAT  
 GAAAACTTAAATTTTTTTTTCTAGGACGAGCTATAGAAAGCTATTGAGAGTATCTAGTAAATCAGTGCAATG  
 TGAAACCTTGTGGTGTATGTGATGTGCTTCTGTGCTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT  
 TCCTTTGATGTCAAGTCTAGTCTATAGGATTGGCAGTTTAAATGCTTTTACTCCCCCTTTTAAATAAATGAT  
 TAAATGTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 38**

MRPGLSFLALLFFLGQAAGDLGDVGPPIPSPGFSFPGVDSSSFSSSRSGSSSSRSLGS  
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV  
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGSSEIVDQ  
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH  
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSQPHPNKGLYWVAPLNTDGRLLLEYRLYNTLD  
DLLLYINARELRITYGQGSGTAVYNNNNMYVNMNTGNIARVNLTTNTIAVTQTLPNAAAYNNR  
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVINTWYTKQYKPSASNAF  
MVCGLYATRMTNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG  
YLLNYDLSVLQKPQ

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**FIGURE 39**

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC  
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT  
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC  
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG  
GAGTATTATAGACTGTACAACCCACTGGATGATTGCTATTGTATATAAATGCTCGAGAGTT  
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA  
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

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**FIGURE 40**

TCTCGCAGATAGTAAATAATCTCGGAAAGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT  
 CCGCTGCTCTTGTGACGTTGTGGAGATGCGGGGAGCGTCTGGGGCTGTGCTCCATGGGGAGCT  
 GGATACCATTTTGTGTGGAAGTGCCCGTGTGGCTATGCCAGTGTCTCCTAGTGGAAAC  
 AACTCCACTGTAACTAGATGTATGCACTTTTCTTGTGTGGAGTATGTGTAGCTTG  
 TGTAAATGTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCTGGATTGTGTGGAATG  
 AGAAAGGCTGTGTCTCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT  
 GGTTTGGCTATGTTCTATCTCTCTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGACATGA  
 TCCTAGAGCTGCACTGCAACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGAACAATTA  
 TTATTGGGGCATTTCTCATTCAGAAAGAACTTTACAACGTGTGTGGTTTTATGTAGGCATG  
 GCAGGTGGCTTTTGTTCATCTCTATACAACTAGTCTTACTTATTGATTTTGACATTCATG  
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAAGGAACTCGAGATGTTGGTATGCAGCCTTGT  
 TATCAGCTACAGCTCTGAATTAATCTGCTGCTTTAGTTGCTATCGTCCGTGTTCTTTGTCTAC  
 TACACTCATCCAGCCAGTTGTTGAGAAAACAGGCGTTTCATCAGTGTCAACATGCTCCTCTG  
 CGTTGGTGTCTCTGTAATGCTATATCTGCAAAATCCAAAGAAATCACAACCAAGATCTGGTT  
 TGTTCAGCTCTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT  
 GAACAGAAACAAATTTGAACCCAACTCTACTAAGCATAATTTGGCTACAATACAACCAAGCAG  
 TGTCCCAAGGAAGGGCAGTCACTGCGTGGTGGCAGTCTCAAGGAATTTATAGGACTAATTC  
 TCTTTTTTGTGTGTGATTTTATTCAGCATCCGTACTTCAACAAATGCTCAGGTTAATAAA  
 CTGACTCTCAACAGTGTGAATCTACATTAATAGAAGATGGTGGAGCTAGAAATGTGGATG  
 ACTGGAGGATGGGGACAGTGTTCCAGGAGCTGTAGATAATGAAAGGAGTGGTGTCACTTACA  
 TATGTTCTCTCTTCTTCACTTCATGCTTTTCTGGCTTCACTTTATATCATGATACCCTTACC  
 AACTGGTCCAGGATGAACCCCTCTCGTGAGATGAAAGTCACTGGACAGCTGTCTGGGTGAA  
 AATCTCTCCAGTTGGATTGGCATCGTGTGCTGATGTTTGGACATCGTGGCACCCTTGTTC  
 TTACAAATCGTGATTTGACTGAGTGTGAGACTTCTAGCATGAAAGTCCCACCTTTGATTTATG  
 TTTATTGAAAACAGTATTTCCCACTTTTGTAAAGTTGTGTATGTTTTGCTTCCCATGTAAC  
 TTCTCCAGTGTCTGGCATGAATTAGATTTTACTGCTTGTCTATTTTGTATTTTCTTACCAA  
 GTGCTTGTATATGAAGTAGAATGAATTTGCAGAGGAAAGTTTTATGAATATGGTGATGAGT  
 TAGTAAAGATGGCCATTAATTTGGGCTTATTTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA  
 ACAAAATTTGTTGACTATTTTAAAAATTAATTAGACCTTAAAGCTGTTTTAGCAAGCATTA  
 GCAAATCTATGGCTGCCCTTTTGAATATTTGATGTGTTGCCCTGGCAGGATACTGCAAGA  
 ATGGTTTTATTTTTAAAAATTTATAAACAACTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA  
 AGGTTTTACCTTTGATACGGAATTTACACAGGTAGGAGTGTTTAGTGGCAATAGTGTAGG  
 TTTATGGATGGAGGTGTCCGTACTAAATTTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA  
 TGGCCCTTTGCCAAAGATGAAGTGTGTTGGTGTGTTTAAACTCATGAAGTATGGGTTCACT  
 GGAATTTTGGAACTCTGAAGGATTTAGACAAGTTTTGAAAGGATAATCATGGGTTAGA  
 AGGAAGTGTGTTGAAGTCACTTTGAAAGTTAGTTTTGGGCCAGCAGCGTAGCTCACCCTT  
 GGTAAATCCAGCAGCTTTGGGAGCTTAAAGTGGGTAGATTACTTGAAGCCAGGAATTCAGACCA  
 GCTTTGGCAGCATGGTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCTGTGGT  
 CAGCAGCTGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGGTTGCACTGAGCAAGT  
 CGTCACTGCACTCTAGCTGGCAGAGATAAGCCAAAAAATATATATATATGAAATCAAGG  
 AGGCAAAATTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGCTACTTAT  
 ATAAATCTAGTCCAGTCTCTCTCATTAAAAAATGAAGACACTGAAATACAGACTTAAAT  
 GCTCAGATGATTAATTAGGAATTTCAAGTTGGCCAATAATAGCATTTCTCTGTACATTTAA  
 AAATAATTTCTTATCAAAATACATGATATGATTTACACCTCATAGTGTGATAATTAATGT  
 GATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAAGAATGATGGAATGTTTT  
 AGAATAAACTCTGCTTATAGTATATACACAGTTCAAAGATGTTTTAAATGCTTTTGTAT  
 TTACTGCGATGATTTGAATATATAGATTATTGTAACCTTTCAACCTGAAATCAAGCAGT  
 ATGAGAGTTTGTGTTATTTGATGTGCTAGTGTCTAATGAAGCTTTTAAATCTCAACAT  
 TCTCTTTTAAAAATTTTAAATGTGAATGGAATGAATAACAATTCAGCTTAATTTCCCAACC  
 TTATCTGTGTGTAGACATTGTATCCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAA  
 ATGAATTCAGAGAAAAA

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**FIGURE 41**

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME  
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSDPRAAVHNG  
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKM  
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYVYTHPASCSENKAFISVNMLLCVGASVM  
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV  
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH  
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVVKISSWIGI  
VLYVWTLVAPLVLTNRDFD

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**FIGURE 42**

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT  
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC  
CCGTGTTTGCTATGCCGATGCTGTCCCTAGTGGAACAANTCCACTGTAAC TAGATTGATCTA  
TGCAC TTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG  
AACAACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT  
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT  
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT  
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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**FIGURE 43**

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC  
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCTAGTGGAACAANTCC  
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT  
GTTGATACCAGGAATGGAAGAACAACGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG  
GTGTTGTCCCTTGTAACATTTTGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG  
GCTANGTTCATNTTCTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG  
AGCTGCAGTGCACAATGGATTTTGGTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG  
GGGC

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**FIGURE 44**

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC  
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT  
TGCTATGCCGATGCTGTCTAGTGGAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT  
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC  
GAATAAGATTCTCGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGTTG  
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA  
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT  
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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**FIGURE 45**

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTCCTTG  
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA  
AGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTGGTTGGC  
TATAAAGCTGTATATCGTTTGTGCTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTACT  
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT  
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACCTTTT  
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACCTAGT  
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA  
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA  
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAAAAACAAGGC  
GTTTCATCAGTGTCACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

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**FIGURE 46**

CTCGGGCGCGCAGGCGAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCGCGCGCGCGCGCGGCTCTCCAAT  
GGCAAAATGTGTGTGCTGGAGGCGAGCGCGAGGCTTCGGCAAGGCGAGTCAGATTGTTGCGACCGGGGCGAG  
TCTCTGAAAGCAGATATAAGAAAACATTTATTAACGTGTCAATCAGAGGGAGCGCCCGCGGGGTGTCCG  
ACTCCGCGCGGAACTTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAAGAGCGGAAAGGCGAGATTAC  
GTCTGTTCCAGCAAGTGGACCTGATCGATGGCCCTCTGAATTTATCAGATATTTGATTTATAGGATGOC  
CCCTGGTTTGTGTGTATCCACACACAGCTGCACACAGGCTCTGGCTCGCTTCCTCTCCCTGTTCCGAGCTOC  
TGGGCGAATCCCACTCTGTTTCAACTCTCCGCGAGGGCGAGCAGGCGCAGAGATGTGTCGAATCTCCGAGTG  
AAGAGGACGAGGGAAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAGAACACCAAT  
CAGCAAAAAAAGAAAGTGGGCCCGCGAGGCTCGTGTGTGCTGTGTCGTCGCACTGTGTCTCCCTGTGG  
TGAAGATCGGTTCTCTGTGCGACCCCGGCTGAAAGGCGAGTTTCAGAGGCGCGCAGGAACATCCGCCCA  
ACATCATCTCTGTTGTGACGGAGACACAGGATGTGAGGCTGGGTTCATGCGAGGTGATGAACAAAGACCGCGC  
ATCATGGAGCAGGGCGGGGCGCACTTCATCAACGCTTCGTGACCACACCCATGTGCTGCCCTCACGCTCTC  
CATCTCATCTGGCAAGTACGTCCACACACACACACCTACACCAACATGAGAATGCTCTCGCCCTCTGTGG  
AGGCACAGCACGAGAGCGCACCTTTGCCGTGTACTCAATAGACTGGCTACCGGACAGCTTTCTCGGGAAG  
TATCTTAATGAATACACGCTCTTACGTGCCACCGGCTGGAAGGAGTGGTGGGACTCTTAAAACTCCCG  
CTTTTATAACTACACGCTGTGTCGGAACGGGCTGAAAGAGAACGCGCTCCGACTACTCCAAGGATACCTCA  
CAGACCTCATCACCAATGACAGCGTGAGCTCTTCCGCGAGTCCAAGAAAGTGTACCGCAGACGGCGAGTCTC  
ATGGTCATCAGGCTCAGGACCGCCCCACGGCTGAGGATTCAAGCCCACAATATTCAGCCTCTTCCAAACGC  
ATCTCAGCACATCAGCGCGAGCTACAACTACGCGCCCAACCGGACAAACACTGGATCATGGCTACACGGGG  
CCATCAAGCCCTCTCAGCATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGCAGCCCTCATGTCCGTTGAG  
GACTCCATGAGACGATTTCACAACTGCTGGTTGAGACGGCGAGCTGGACACACGTCATCGTATCAACCCG  
CGACAGACCTGTTACCATCTGGCCAGTTTGGCTGGTGAAGGGAATCCATGCCATATGAGTTTGAATCAGGG  
TCCGCTTCTAGCTGAGGGGCCCAACGCTGGAAGCCGCTGTCTGAATCCCACTCGTCTCAACATGAGCTG  
GCCGCCACCTCTGGACATCTGAGGCTGGACATACCTCGGATATGGACGGGAATCCATCCTCAAGCTGG  
GGACAGCGAGCGCGGTGAATCGGTTTCACTTGAAGAAAGAAAGTGAAGGTGTGGCGGACTCTTCTTGTGTG  
AGAGACGCAAGCTGCTACACAAAGAGAGCAATGACAAAGTGGACGCCAGGAGGAGAACTTTCGCCCCAAGTAC  
CAGCGTGTGAAGACCTGTGTACGCTGTGAGTACGAGCGGCTGTGAGCAGCTGGGACAGAGTGGCAAGT  
TGTGAGAGCGCCACGGGGAAGCTGAAGCTGCATAAGTGAAGGGCCCATGCGGCTGGCGGCGACGAGCGCC  
TCTCAACCTCTGTCGCCAAGTATCTACGGGCGAGGCGAGGCGCTGCACTGTGACAGCGGGGACTACAAGCT  
AGCCTGGCGGGACCGCGAAATACTTTCAAGAAAGATGACAAGGCCACTATGTCCGCACTGCTCCCTCCG  
CTCAGTGGCCATCGAGTGGACGGCGAGGCTGACACGCTAGGCTGGGTGTGCGGCCAGCGCCGAAACCTCA  
CAAGCGGCATCGCCAGGCGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGG  
CTTCCGCACTACTCAGCCGCCAACCCCATTAAGATGACACATCGTGTCTACCTAGAGAAGCAGACGTCGA  
GTGTGACCTGGCCCTGTACAGCTCCCTGAGGGAAGTCCGAGGTCACTGAAGAAAGCGGCGCAGATATGTGAC  
CCCTGCAGAACCAAAATTAAGAACTGAGGGAAGTCCGAGGTCACTGAAGAAAGCGGCGCAGATATGTGAC  
GAGGACCTGCAAGAGGAAGGACAGGTGTGGCTGTTTGGGGAGCAGAGCGCAAGAAAGAACTCCGCAAGCTGC  
TCAAGCGCTGCGAACAACGACACGCTGCGAGCATGCCAGGCTCAGCTGCTTCAACCAACGACCAACGACTGG  
CAGACGGCGCTTTCGACACTTGGGGCTTCTGTGCTGCTGACAGCGCAACATAACACGTACTGTGTCAT  
GAGGACCATCAATGAGCTCACAATTTCTCTTCTGTAATTTGAACCTGGCTCTAGAGTCTTTGATCTCA  
ACACAGCCCTTACAGCTGATGAATGCAAGACACTGACAGGAGTGTCTCAACAGCTACAGCTACAGTCA  
CTCATGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGAGCACTGGATGGAG  
AAGCTATGACCAATACGCGATTTCAGCTGGAAGTGGCCAGAAATGAAGAGACTTTCTCAAACTCACTGG  
GACACCTGTGGGAAGCTGGGAAGGTGAAGAAACACAGAGGTGGACCTCAAAAGATAGAGGATCACTGTA  
TGTCAAGCAACATGAAGAAACCTGTGGGTGATTTCCAGCAAGCTGTGCTATTTGGCCAGGAGGCTGAGAAG  
AAGCAGCAGCTTCAGTCAACATGACAGATTCTGGAGGATAACGACAGAGGACAGAGATAACTTCAGGAAGTCC  
ATTTTTCGCTGCTTTTGGCTTTGGATTATACCTACAGCTGACCAAAATGCAATTTTTCGATCAAAAGTCC  
ACCACTAAACCTCCCCAGAAGCTCACAAGGAAACGAGAGAGCGAGCGAGAGAGATTTCTCTGGAAATTTCT  
TCCCAAGGGGAAAGTCTTGAATTTTAAATCATAGGGGAAAGCAGTCTGTGTTCTTAAATCCTCTTATTTCT  
TTGGTTTGTCAAAAGAGGAATTAAGAGCAGGACAGAGGCAACGTGGAGAGGCTGAAACAGCTGCAGAGCG  
TTTGCAATGAGTCAGTGAAGAAAGAGATGACATTTACCTAGCACTATAAACCTGGTTGCCCTGAAGAAA  
CTGCCTTCATTGTATATATGTGACTATTACATCAACATGGGAATTTTAGGGGAACTATAAGAAAT  
CCCAATTTTCAGAGTGGTGGTCAATTAACGCTGTGGCCAGTGTAAAGAAAA

**FIGURE 47**

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ  
VMNKTRIMEQGGAHFINAFVTPMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE  
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD  
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP  
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT  
YIVYTADHGHHIGQFGLVKGKSMPEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI  
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN  
FLPKYQVRKDLQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY  
YGGGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAQ  
PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS  
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKRPCECDCHKISYHTQHKGRLKHRGSSL  
HPFRKGLQEKKDKVLLREQKRKKLRLKLLRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG  
PFCACTSANNNTYWCMTINETHNFLCFEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL  
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

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**FIGURE 48**

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA  
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC  
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACC  
TGCCCTTTTCCACGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA  
CCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGCGGGGCCACCTGGGAATCTTTCACC  
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC  
CCCCGCCACACCCCTCACCACTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA  
CGCTCGCTGAAGGCTGCTGTCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG  
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG  
GGAACAATAGACTGGGGCTTGTCCAGCTGCATTGTCATGGCATGCCCAGTGTACTATGGC  
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGGTTTGGGGAGTGGAGAGCAAGG  
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG  
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC  
ATCAGGCTGTGCAGGCCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAAATGTCTTTT  
GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTCATCGGTGCCTTAGTCCAAGAAAAT  
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 49**

MLGLLGSTALVGWITGA AVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFR  
RRGHLGIFHHHRHPGHVSHV PNVGLHHHHHPRHTPHHLHHHHHPHRRHHPRHAR

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**FIGURE 50**

GCGGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCCATGTCGGACCTGCTA  
 CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGACGCTGCTGGCCTTTGCCGG  
 GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCATCCGCAACGTCA  
 CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC  
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC  
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC  
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC  
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG  
 TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATCCTCGGCTGG  
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT  
 GTGCCGTGAGATGAAGGAGACAGAGTGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA  
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACAGTTCTGTAAAGCTTGGAAAGTGAGCC  
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGGGGCGAGCAGCCGTGGCTGGGAT  
 GACGGTGACACCCGACGAGCAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA  
 GGAGCTGGACTTGAGGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC  
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAGTAACCC  
 ATGGCCTGCACCTCTCTGCAGTGCAGTTGCTGAGGAAGTGAAGCAGACTCTCCAGCAGACTCT  
 CCAGCCCTCTTCTCCTTCTCTGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC  
 TCCAGGCCCTTGTCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA  
 GGGACTATTTTCTGCACACAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTCAGACTC  
 ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAA  
 AAAAAAAAAA

**FIGURE 51**

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR  
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRAVGSI LSEGEESPSPELIDLYQKFGFKVFS  
FPAPSHVVTATFPYTTILSIWLATTRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCP LAR  
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS  
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK  
GKE

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CCCGGGGAACGCTGTCTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT  
GCCCCGCGCCAGTCA**ATG**ACCTTGCGCCCTCACTCTCCCGCTCCATCTGCTGCTGCTGCT  
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA  
CCCTCCAAGTGGAGACCTTGGTGGAGCCCCAGAACCATGTGCCAGCCCGCTGCTTTTGGA  
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT  
GACCAGAGACCTCTGGTTATAGAACTTGCCCAAAGACAGGTGATTCAGGCTCTGGAGCAGA  
GTCCTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTCTCTCACTTGGCCTAT  
GGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGT  
GATTGCACATATCCGAGCCAACTACTGGCTTAAAGCTGGTGAAGGCGCATTTTGCCTCTGGTAG  
GATGGCCATGTGTGCAGCCCTCTGGGCTCATTTGGTATACCTTATACGAAAGGCCAAT  
AGACCCAAAGTCTCCAAAAAGAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAAT**A**  
**ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA**

**FIGURE 53**

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI  
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF  
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS  
KKKLKEEKRNKSKKK

**FIGURE 54**

CCCGGGAACGTGTTCTCTGGCTGCCGCACCCGAACAGCCTGTCTCTGGTGCCCCGGCTCCCTGC  
CCCGCGCCAGTCATGACCCTGCGCCCTCACTCTCCCGCTCCATCTGCTGCTGCTGCTGC  
TGCTCAGTGCGGCGGTGTGCCGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC  
CTCCAAGTGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA  
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA  
CCAGAGACCCTCTGGTTATAGAACTTGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT  
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG  
AAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA  
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG  
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA  
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA  
AATAATAAATTTTAAAAAAGCTTA

**FIGURE 55**

CCGAAAGTCCCGTCCGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCC  
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG  
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA  
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT  
CCTTCTCACTTGGCCTATGGAACCGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT  
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG  
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC  
CTATACAGAAAGGCCAATAGACCCAAAGTCTCAAAAAGAAGCTCAAGGAAGAGAAACGAAA  
CAAGAGCAAAAAGAAATAATAAATAATAATTTAAAAAACTTAAA

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**FIGURE 56**

CTGCTGCATCCGGGTGCTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGGAG  
 TGAGCGGGGCGGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG  
 ACCTGAAAAAAATGCTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG  
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT  
 TATCATAGATGCAGCTGTTATTTATCCCAACCATGAAAGATTTCAACCACTCATACCATGCCT  
 GTGGTGTATAGCAACCATAGCCTTCTTAATGATTAATGCAGTATCGAATGGACAAGTCCGA  
 GGTGATAGTTACAGTGAAGGTTGCTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTGG  
 TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG  
 CTAAAGAAAAAGACATAGTATACCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT  
 TTTGGAGGGCTGGTTTTTAAGTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT  
 TTCCACAGCACAAACAGCCCTGCATGGGTTGTTTGTTTTTTACTGCTCACTCCCAACCTT  
 TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT  
 AAAATCACGAGAACCTTAAACAACAACCAAAAATCTATTGTGGTATGCACCTTGATTAACCT  
 ATAAAAATGTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT  
 TGAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA  
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT  
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCCGTGG  
 TCAAAATCTTCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT  
 GTAACTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT  
 GGTCCAGCCACCAGGCTCCCTGTGTCCTTCCATGGGAAGGTCTCCGCTGTGCCTCTCAT  
 CCAAGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC  
 ACATCCACCACTG

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**FIGURE 57**

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI  
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK  
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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**FIGURE 58**

TTCTTGGCTAAAATCGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC  
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG  
CTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGATC  
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT  
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC  
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG  
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG  
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAGACATAGTATACCCTGGAATGCTGTATT  
TTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGTTTTTAAGTTTGGC

**FIGURE 59**

TGGACGGACCTGAAAAAAATGTTTGGATTNTAGAGGGNTTGAGATG TTCAGAATGCATGAC  
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG  
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTCAACCANTCATACC  
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA  
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT  
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT  
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC  
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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**FIGURE 60**

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAAATGTTGGATT  
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT  
CCATTGCTGCTGGTGACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT  
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC  
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT  
GTTTGGGTCAAAACAGGTGNTCGCATTGCGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATT  
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAGACATAGTAT  
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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**FIGURE 61**

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC  
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT  
ATCCCACCATGAAAGATTNNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC  
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG  
TTTGGGTCAAACAGGTGNTNGCATTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN  
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC  
CCTGT

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**FIGURE 62**

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGGCGCGG  
CGNGACACCGGGTTCCGGGAACCATTCACGACGGGGTGGACTGACCTGAAAAAATGTTTG  
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT  
GCTTCCATTGCTGCTGGTGACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT  
TATTTATCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA  
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA  
GGTTGCTCGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG  
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG  
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

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**FIGURE 63**

CGACGCCGGCGT**GATG**TGGCTTCCGCTGGTGTCTCTCTGGCTGTGCTGTCTGTGGCCGTCC  
TCTGCAAACTTTACTTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCGGAAGATGTC  
AAACGCCCCAGCGCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTCTCAAAACAAGC  
TTTTCTCAGCGCAACCAAGTCCCGGAGAAGCTGGATGTGGTGGTAATTTGGCAGTGGCTTTGGGG  
GCCTGGCTGCAGCTGCAATTTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGTCTGGGAACAACAT  
ACCAAGGCAAGGGGCTGCTGTACATACCTTTGGAAAGAAATGGCCTTGAATTTGACACAGGAAAT  
CCATTGACATTTGGGCTATGGAAAGAGGCGACATTTGGCCGTTTATCTTGGACGAGTCACTG  
AAGGCGCATTTGGACTGGGCTCCCCCTCTCTCTCTCTTTTGACATCATGGTACTGGAAGGGCCC  
AATGGCCGAAGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTCAGGGCCTCAAGGA  
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA  
GTGGAGCCCTCATGGCCATCCTGTTGAAATTCCTCCATTGCCCGTGGTTCAGCTCCTCGAC  
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTTCAAGCATCCACCAGAGCCTGGCTGA  
GGTCTCTGCAGCAGCTGGGGGCTCTCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA  
CTTACGGTGTCAACCCCAACCAAGTGGCTTTTCCATGCACGCCCTGCTGGTCAACCACTAC  
ATGAAGGAGGCTTTTATCCCCAGGGGGTTCAGTGAAATTTGCCCTCCACACCATCCCTGT  
GATTACAGGGGCTGGGGGCTCTCTCTCAAAAGGCCACTGTGCAGAGTGTGTGTCTGGACT  
CAGCTGGGAAAGCCTGTGGTGTCAAGTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC  
CCCATCGTGGTCTTCCAAAGCCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAAGCG  
CCGCTGCCCTGCCAGTGTGAAGCAGCAACTGGGGACGGTGCGGCCGGCTTAGGCATGACCT  
CTGTTTTATCTGCTGCCAGGACCAAGGAAGCACTGCATCTGCCGTCACCACTACTACT  
GTTTACTATGACACGGACATGGACAGGCGATGGAGCGCTACGTCCTCATGCCAGGGAAGA  
GGCTGCGGAACATCCCTCTCTCTCTCTCTCTTCCATCAGCCAAAGATCCGAGCTGGG  
AGGACCGATTCCAGGCCGCTCCACCATGATCATGCTCATACCCACTGCCACGAGTGGTTT  
GAGGAGTGGCAGCGGAGCTGAAGGGAAGCGGGCAGTGCATGAGACCTTCAAAAACCTC  
CTTTGTGGAAGCCTATATGTCACTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGG  
AGAGTGTGACTGCAGGATCCCCACTCACCACCAAGTTCATCTGGCTGTCTCCCGAGGTGGCC  
TSCATCGGGCTCCCATCAGCTGGGCCGCTGCACCTTGTGTGATGGCTCTCTTGAGGGC  
CCAGAGCCCCATCCCCAACCCTATCTGACAGGCCAGGATATCTTCACTGTGGACTGGTGC  
GGGCCCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCTGAAGCGGAACTTGTACTCAGAC  
CTTAAGAATCTTGATTTAGGATCCGGGCACAGAAGAAAAAGAA**TAGT**TCCATCAGGGAGG  
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG  
CATTAGTTCTTTGACGATATAAAGCACTCTAATTTGGTTCTGATGGCTGAAGAGAGGCCCTAG  
TTTTAAATCACAATCCGAATCTGGGGCAATGGAATCACTGCTTTCAGCTGGGGCAGGTGAGA  
TCTTTAGCCCTTTTATAACATGCCATCCCCACTAATAGGATTTGACTTGGATAGCTTGATG  
TCTCATGACGAGCGGGCTCTGCATCCCTCACCATGCCTCTCACTCAGTGATCAAGCGGA  
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGAGCTCAACCTGGTGGGTCTAGTTCT  
TGTCTCAGGCTCTGTCTCTATTCTTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG  
GAAAGAGGAGACTAATAGGCTTAACCTAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA  
GGTGTGAGAGCTCTAGATCTCTTTTGTGCTGGTTTCACTGGCTTCTAGGCTTCTATCTTATCA  
GCCGTGTCTGTGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA  
GGGTGCATGCAGATGATCATCCAAATCATATGGAAGTCCGGGTCTGTCTTCTTATCA  
TCGGGTTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCCTCAATCAAGC  
CTTATCCACCAATACACAGGGAAGGTGATGCAGGGAAGGTGCATCAGGAGTCAAGGATCAGGGA  
TGGAGCTGGTAAGATGAATCTTTGCTGGGCTGAAGCAGGCTCAGGGGCATTCCAGCCAAGGG  
CACAGCAGGCGACAGTGCAGGAGGTGTGGGTGAAGGAGGGAAGTCAATCAGAAAAGGGA  
AAGCCAGGAAATGTGTGAAGCCAGAAATGGCAATTTGCAGTTAATTAGCACATGTGAGG  
TTAGCAGGTAGTGGATCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGTCTTTG  
GTATCAGACATCGAAAGGTCTCTTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATTG  
ATTCCATTGCTTTAAAAA

**FIGURE 64**

MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSSEVDKRPPAPLVTDKARKKVLKQAFSAN  
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG  
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ  
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ  
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA  
GGAVLTkATVQSVLLDSAGKACGVSVKKGHELNIYCPiVVSNAGLFNTYEHLLPGNARCLP  
GVKQQLGTVRPGLGMTSVFICLRGTEKEDLHLPSTNYYVYYDTMDQAMERYVSMFREEAAEH  
IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEA  
SMSVVLKLFPPQLEKGVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI  
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

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**FIGURE 65**

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA  
 GGGGTTGGCACCGGCCCCGAGAGGAGGATGCGGCTCCGATAGGCTGACGCTGCTGCTGTG  
 TCGGTTGCTGCTGAGCTTGGCTCGGCTCCTCGGATGAAGAAGCAGCCAGGATGAATCCT  
 TAGATTCGAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA  
 GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGAATTAGAATCCTCTATTCAAGA  
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG  
 AGTCTCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAACACAGCTTTG  
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTCTTAGATAA  
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT  
 ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCTAAGAGA  
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAAGTGAATGAAATCCTTAATGGAAGCAA  
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTGGTGATTACTTGCCACAGAATATC  
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGAGTGC  
 TCTTGCTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAAGGCTCTTGAT  
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTGGTAAGTAGACTT  
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTT  
 TCAGCTTTCATGATCCAGATTTGCTTGATTAAGACCAATATTCAGTTGAACCTCCTTCAA  
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACA  
 ATTTTCTTTAAATTTGATTAGTTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC  
 TCTTTTAAATTTTCTCTGAGTTGGAATTTGTGAGAATCATTTTTTACATTAGATTATCATAA  
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT  
 GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT  
 GTGCAGAATGACTCCAGAGAGCTCTACTTTCTGTTTTTACTTTTTCATGATTGGCTGTCTTC  
 CCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCTTCCAGTAGTCTCATTTTCC  
 CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACATTTTTTAATAAA  
 ATTATGTCTAAGATTAAAAA  
 AA

**FIGURE 66**

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD  
SESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHG  
EPCHFPPFLFLDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMGEAEMM  
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMFEK  
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

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**FIGURE 67**

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT  
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT  
GTCAGTTTCCAGACAGTCTTGGCCCAGCTGGATGCACTGCTGGTCTTCCAGGCCAAGTGG  
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCTCTGG  
TACCAGCAGCGGGCAGGCAGTGCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA  
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCAATGCCT  
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC  
TACGGCTTTAGTCCCTAGGGGTGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT  
GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGG  
TTAATAATATTCAACATGTCAACAAC

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**FIGURE 68**

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG  
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSF

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**FIGURE 69**

GCGCGCCCGCCCGAGACCGGGGCCCGGGGCGCGGGGCGCGGGATGCGCGCCCGGGGCGGG  
 CGATGACCGCGGAGCGCAGCGCGCGGGCCCGGCCCTGACCCCGCCGCCCGCCGCTGAGCCCC  
 CCGCGCGAGGTCCGGGACAGGCCGAGATGACGCGCGAGCCCGCTGTTGCTGCTCCTGCTGCGCG  
 CGCTGCTGCTGGGGGCCCTTCCACCGCGCGCGCGCGCGCGAGGCGCCCCAAAGATGGCGGAG  
 AAGGTGGTCCACCGCAGGTGGCCCGCTGGGCGCACTGTGCGGCTGCACTGCCAGTGGAG  
 GGGGAGCCCGCGCGCGCTGACCATGTGGACAAAGATGGCCGACCATCCACAGCGGCTGGA  
 GCGGCTTCCGCTGCTGCGCGAGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGGC  
 GTGTAGTGTGAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCTCGTCTGT  
 GCTGGATGACATTAGCTCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCCTTGGGGGTCAAG  
 AGGACCCCGCAGCCAGCAGTGGGCACGACCGCGCTTACACAGCCCTCCAAGATGAGGCGC  
 CGGCTGATCGCAGCGCCCTGGGTAGCTCCGTGCGGCTCAAGTGGTGGCCAGCGGGCAGCC  
 TCGGCGCGACATCAGCTGATGAAGGACGACCAAGCCTTGACGCGCCAGAGGCGCGTGGAG  
 CCGGGAAGACAGTGGACACTGAGCCTGAAGAACCTGCGGCGGAGGACAGCGGCAATAC  
 ACCTGCCCGCTGTGAACCGCGCGGGGCCCATCAACGCCACCTACAGGTGGATGTGATCCA  
 CGGGACCCGTTCCAAGCCGTGCTCACAGGCACGACCCCGTGAACACAGCGGTGGACTTCG  
 GGGGACCCGCTCCTTCAAGTGAAGGTGCGCAGCGCAGTGAAGCCGGTGTATCCAGTGGCTG  
 AAGCGCTGGAGTACGGGCGCGGAGGGCGGCCAACCATCGATGTGGGCGGCCAGAA  
 GTTTGTGGTCTGCCCCAGGGTGACGTGTGGTTCGGGCGCCAGCGGCTCCTACCTCAATAAGC  
 GTTTCATCACCGTGGCGCCGAGGACGATGCGGCGATGTACATCTGCTTGGCGGCCAACCC  
 ATGGGCTACAGCTTCGCGAGCGCTTCTTCAACCGTGTGCCAGACCCAAACCGCCAGGGGCC  
 ACCTGTGGGCTCCTGCTCTCGGCACTAGCCTGCGCTGGCGCGTGCATCGGCATCCAG  
 CGGCGCTGTCTTATCTTGGGCACCTGCTCCTGTGGCTTTGCCAGGCCAGAGAAGCGC  
 TGGACCGCCCGCTGCCCCCTCCTTCTGCTGGGCACCGCCCGCGGGGACGCGCGGACCG  
 CAGCGGAGACAGGACCTTCCCTCGTGGCGCGCTCAGCGCTGGCCCTGGTGTGGGCTGT  
 GTGAGGAGCATGGGTCTCGGCGAGCCCGCAGCACTTACTGGGCGCAGGCGAGTGTCTGGC  
 CCTAAGTTGTACCCCAAACCTCTACACAGACATCCACACACACACACACACATCTCACAC  
 ACATCTCACAGTGGAGGGCZAGGTCCACAGCAGATCCACTATCAGTGCATAGACGGCACCGT  
 ATCTGCACTGGCAGCGGGGGGCGCGCGCAGACAGGACAGTGGGAGGATGGAGGACGGAGCT  
 CGACAGCAGAGTGGGAGACCATGGCGAGGAGGAATGGCCAGACCCAGGACGATCTGTGTG  
 TGAGGCATAGCCCTGGACACACACACAGACACACACTACCTGGATGCATGTATGCAC  
 ACACATGCGCGCACACGTGCTCCTTGAAGGCACACGTACGCACACGACATGACACAGATG  
 CCGCTGGGCACACAGATAAGCTGCCAAATGACAGCAGCAGCAGACAGAGATGCCAGAAC  
 TACAGGACATGCTGCTGAACATACACAGCAGCAGCCATGGCGAGATGTGCTGCTGGAC  
 CACACACACACAGGATATGCTGTCTGGACGCACACAGTGCAGATATGGTATCCGGACAC  
 CAGCTGCACAGATATGCTGCTGGACACACAGATAATGCTGCTTGACACACATGCAACGG  
 ATATTGCTGGACACACACACACACACAGCGGTGCACAGATATGCTGTCTGGACAGCAC  
 ACATGCAGATATGCTGCTGGACACACACTTCCAGACACAGTGCAGGACAGATATGCT  
 GCCTGGACACAGCAGATATGCTGTCTAGTCACACACACAGCAGCATGCTGTCCGGACAC  
 ACACAGCATATGCAGATATGCTGTCCGGACACACACAGCAGCAGATATGCTGCTGGAC  
 ACACACAGATATGCTGCTGCTCAACACTCACACAGTGCAGATATGCTGCTGGACACAC  
 TGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATATGCTGTCCGGATACACAG  
 CAGCAGACAGATGCAGATATGCTGCTGGGCACACACTTCCGACACACATGCACACACAGT  
 GCAGATATGCTGCTGGACACACACAGATAATGCTGCTCAACACTCACACAGTGCAGAT  
 TATTGCTGGACACACACATGTCAGAGATATGCTGTCTGGACATGCACACAGTGCAGATA  
 TGCTGTCCGGATACACAGCAGCAGACATGACAGATATGCTGCTGGGCACACACTTCCGGA  
 CACACATGCACACAGGTGCAGATATGCTGCTGGACACAGCAGACTGACGCTGCTTTGG  
 GAGGCTGCGGTGAAGCTGCAGTACGTGTGCGTGGGCTCATGTTGATGAGGAGGCTTT  
 CCCTGCTCCACGCTCACTCCCCAACTTGCGCCGCTCTGTCCCGCTCAGTCCCCCGGCTT  
 CACTCCCGCTCTGTCCCCGTGGCCTTGGCGGCTATTTTGGCCACTGCTTGGGTGGCCAGG  
 AGTCCCCCTAGTGTGTGGGCTGGGGTGGGGGACAGCAGCCCAAGCCTGAGAGGCTGGAG  
 CCGATGGCTAGTGGCTCATCCCCAGTGCAATTCCTCCCTGACACAGAGAAGGGGCTTGGTA  
 TTTATTTTAAAGAAATGAAGATAATATTAATATGATGAAGGAAGACTGGGTGTCCAGGAG  
 TGTGTTCTCTCTGGGGCGCGGACCCCGCTGGTCTTTACGACATGCTGATGACCAACCCC  
 GTCCAGGCCAGACACCACCCCACTGCTGCTGGTGGCCAGATCTCTGTAAATTTTA  
 TGTAGAGTTTGAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACAAAA

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**FIGURE 70**

MTFSPLLLLLLPPLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM  
WTKDGRTIHSWRSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK  
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIA R PVGSSVRLKCVASGHPRPDITWMK  
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL  
TGTHPVNTTVD FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLP TGD  
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA  
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS  
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV  
HQHIHYQC

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[illegible]

**FIGURE 72**

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPISIFAKPADTLESPEGWTTWFNI  
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQ  
 RPGQNCSDNYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMSVLCS  
 EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK  
 TPKLLTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTPKTSLKAATIKAEFVRAETPY  
 MVMNPETKARRAGQSVSLCKKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAG  
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQATNSFYVDVGRCPV  
 KTCAGQQDNGIRCRDAVQNCGGISKTEEREIQCSGYTLPTKVAKECSCQRCCTETRSIVRGRV  
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVFPQDTERLVLTFFVDRQLQKFVNTTKVLPFN  
 KKGSVAFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV  
 KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL  
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL  
 DVPESRRCFVKVVRAYRSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGNGA  
 CVPAFCDQDQSPDAYSAYVLASLAGEELQAVESSPKFPNPAIGVPQPYLNKLNRYRRTDHDPR  
 VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPFN  
 EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS  
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVVIPOGSCRRASVNPMLEHYLVNHLPLAV  
 NNDTSEYTMPLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT  
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGQRQGGVVASLRFPRVA  
 QQPLIN

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**FIGURE 73**

CTGCAAGTTGTTAAACGCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCAC  
 AATATCTTAACCTCTCATATTTGGTTTGGGATCTGCTTTGAGGTCCCCTCTCATTTAAAAAAAATACAGAG  
 ACCCTACCTACCGTAGCCGATACATATGTATATATATGTAACTAGACAAGATCGCAGATCATAAAGC  
 AAGCTCTGCTTAGTTTCTCAAGAAAGATTACAAAGAAATTTAGAGATGATTATTGTCAAGATCCCTGTGCGATTGATG  
 CCCCTTTGGGTTACGCTGTCCCTCAGTGATGCGGCCCTACCCCTTTGGTTTGGGGACATTTGATTGTGTAAGACT  
 CAGATTTACACGGAAGAAGGGAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAAATA  
 TCTGAAAGTGAACCTCGATCTCCGGATATTACCTGTGGAGACCTCTCGAGACCTCTGTGCAATGGGCATC  
 CCTACATGTGCAATAATGAGCTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTGATT  
 GAAGGAAGCATCCCTCCACATTTTGGCAGTCTGCCACTTGGGAAGGATATCCCAAGCCTCTCCAGGTTAACT  
 CACTCTGCTTGGAGCAAAACCATTTGAGCTAACAGACACATAGTTATTACCTTTGAATCTGGGCTCCAGACC  
 AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGATGCTTA  
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTTATCACAGCATACGGTCTTAGAAATCATTTGCACAGA  
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATATTCACCTTTGAAATCAAAGACAGGTTCCGCGCTTTTG  
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT  
 ACAGTCAAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAATAATTTGTAGATGAGCTACACTGGC  
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTTCCATGCCACTGTATGTG  
 TGTATGACAACAGCAAAATGACATGCGAATGTGAGCACAACTACAGGTCCAGACTGTGGGAAATGCAAGAAG  
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCAAGGCACTGCAAAATACCTGTATCCC  
 CAGTATTTCCAGTATTGGTACGAATGTCTGCGACAACAGAGCTCTGCACTGCCAGAACGAGGAGCTGCCACA  
 ACAACGTGCGCTGCTGTGCCCCGCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTCCGAGAGGCTGGC  
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCGCGACGGCACCCAGCGCTGCTGCTGCTGACCAAGCTGGT  
 GGGAAACGCCAGCCCTTGGTGTCTTAGGTGTACCTCCAGGCCACACGGGACGGGCTGTGCGGTGGGGAAGCA  
 GACACAACCCAAACATTTGCTACTAACTAGGAAACACACATACAGACACCCCACTCAGACAGTGTACAAA  
 CTAAGAAGGCCCTAAGTGAACCTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTT  
 TGACTCCAGAGGAGTTGGCAGCTGTGTATTTATCTACTGCAAAATCAGATTTGCCAGCTGACAGCATATTTGGGA  
 TTGGAAAGGCTGCGACAGCCCCCAACAGGAAGACAAAAACAAACAAATCAACCGACCTAAAAACATTTGGC  
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACAAATAGCATTTCTTGTCTGTCAG  
 TCGCATTTGGGCAATAAGGAATCTGTACAGCTGCCATTTGGCCTGCTTCCGTCCCTGATCCCTTCCAAC  
 CTGTGCTTTAGTGAACGTTGCTCTGTAACCTCGTTGGTTGAAAGATTTCTTGTCTGATGTTAGTGATGCA  
 TGTGTAAACAGCCCTCTAAAAGCGCAAGCCAGTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTCCGA  
 GCACACACCACTATACAGAGTGGCTATAGGAAAAAGAAAGTGTATCTACTCTTTGTATTCAAATGAAGTT  
 ATITTTCTTGAACCTACTGAAATAGTAGATTTTGTATTTATGCAATTTGTGTACCAGACAATCTGTTAAT  
 GTAICTAATTCGATACAGACAGACIGACATTTTATTTTCTCTCTTCTGTTCTGTTTGTTCATCTGGGACA  
 GATTTCTCTGTAGGGCAAGCAAGCGTCTGGCATCAAGAATATCAGTTTACATATATAACAAGTGTAAATAA  
 TTCCACCAAAAGACATTTCTAAATGTTTTCTTGTGCTTTTAACTTGAAGATTTAAAGATAAAAACTCTGCA  
 TAAACGATTTTCAAGATTTGTATGCAATTTCTTAAGATGAAGGAACAGCCACCAAGCATTTCACTCACT  
 TTAACGATTTCTGTGGACTGAGTACATTCAGCTGACGAATTTAGTTTCCAGGAAGATGAGTTGATGTCACT  
 AGCTTGGACAACTTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATACACAGCAAAAAA  
 AAAAAA

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**FIGURE 74**

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK  
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK  
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMIKSLDYGRTWQPYQYYATDCLDAF  
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD  
TTKKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN  
SKLTCECEHNTTGPD CGKCKKNYQGRFWSPGSYLP I PKGTANTCIPSISSIGTNVCDNELLH  
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTLLGTAS  
PLVF

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CCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGTCCGCTAAGATTGCTGAGGAGCGCG  
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCCGCTCCGGGCAGAGTGTCTCATGACTT  
CTCTTGTGGACCA**ATG**TCCGTGATCTTTTTTGCTGCGTGGTACGGTAAGGGATGGACTGCC  
CCTCTCAGCCTCTACTGATTTTTACCACACCCAAAGATTTTTTGAATGGAGGAGACGGCTCA  
AGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTT  
AGTATACATTTTTCTTCTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC  
AGCAGCCTATGGCCTTCTGCTTCTCGGAGACCTGTGGTGGGAATTCACAGCTTCCTATGACA  
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTAG  
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT  
TCAGGAGGAGCTCAAGTTCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA  
ATGGGGTGATGAATGGTCACACACCGATGCACCTTGGAGCCTGCTCCTAATTTCCGAATGGAA  
CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTTCTAACATCATGTGTGCTGCCCTGAATCT  
CATTGAGGAGGTTACACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCGTCTGGT  
TGGACCAAACTCTG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT  
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGAGCCTGTGGA  
AAAGGGCATGTGAGTGAAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG  
ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTAGGGTAAAAATTAACAAATCCATTCTAT  
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT  
GCTTCAGAAGTGTTATTTTCATGAATCATTTCATATGATTTGATCCCCAGGATTCATTTTGT  
TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT  
TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTCT  
TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAACTCAGTAGTACAAC  
TAAACTTGATATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAAATTAATG  
AAGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAATAAAAAAAAAAAAAAAAAA  
AAAAA

**FIGURE 76**

MSVIFFACVVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF  
SSFGDVACMAICSCQCPAAMAFCFLET LWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW  
HFNYVSSQMECSLEKIQEELKLQPPAVLTLED TDVANGVMNGHTPMHLEPAPNFRMEPVTA  
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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**FIGURE 77**

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT  
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTGAGAAAGTGAAGTGGCATT  
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG  
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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**FIGURE 78**

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAAACGTAGCGCGA  
 CCCGACCTTAAAGAGTGGGGAGCAAAGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG  
 CCTGCCCCCTTAAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT  
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCTT  
 CCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA  
**TGGAAGCACTGACTACGAAGTGCTATCCGTGCGGAGAACAGCTATTCCACGAGAGGATCCGC**  
**GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTCTGAC**  
**CCGCTTCAAGAAGCCTGCTGAGTTACCACAGTGGATGATGAAGATGCCACCCTCAACAAGA**  
**TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTCTCTGCCCC**  
**TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCTCGGAACACTACATCCAGTGGCT**  
**CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA**  
**TCTTCCCTCATGCCCTTTCATATTTCTTCACTGAGTCTGAGGGCTTGTGTGGCTCCAGAAAG**  
**GGTGTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGTCT**  
**AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAGGGCCACAGAGAGTCACTCT**  
**ATGACTTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCCCTGGGGTTCTG**  
**CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCGCATGTTCTCCGTCACTGGGAAGCTGCT**  
**AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG**  
**CAGCCCTGACCCCGAGGATCTGTAATCCTACTTCCCTGCTGGCTGCTCTTAGACATGGAGCTG**  
**CTACACAGACAGGTCCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGGCGGAAGGC**  
**TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGTGGTGTGACGG**  
**GCCTGTCTGTGCTCATTGTGGCCATCCACATCTCTGGAGTGTCTCATCGATGAGGCTGCCATG**  
**CCCCGAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG**  
**TGCCGTCAATCAGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTATA**  
**GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCAGACACTGCCATGACGCAGATAATT**  
**GGGAAGTGTGTCTGTCTCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGG**  
**GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTCTACA**  
**TTGTGTCTCTACAAACGAGCCTTTGCAGGCCCTCACCACACTCTGTCTGGTGAAGACCTTC**  
**ACTGCAGCTGTGCGGCAGAGCTGATCCGGGCCCTTTGGGCTGGACAGACTGCCGCTGCCCGT**  
**CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACAGTGAACCTCCAGCTGGGGGTGGGA**  
**AGGAAAAAAGTGGACACTGCCATCTGTCTGCTAGGCCCTGGAGGGAAGCCCAAGGCTACTTGG**  
**ACCTCAGGACCTTGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCATATT**  
**GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCTGTCTTTCCATACTTAACTGTGGCCT**  
**CAGCATGGGGTAGGGCTGGGTGACTGGGTGATGCCCTGATCCCAAATCTGTTTACACATCA**  
**ATCTGCCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT**  
**AGGGTGGGGTAGGGGAGGGAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC**  
**CTGTGCTCTGGCCCTCAGCAGCCTAAGCACTGTGCTATCTGTGAGGGGCTTTGGACCACTG**  
**AAAGACCAAGGGGATAGGGAGGAGGAGGCTTACGCCATCAGCAATAAAGTTGATCCCAGGGA**  
**AAAAAA**

**FIGURE 79**

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK  
IALELCTFTLAIALGAVLLLLPFSIISNEVLLSLPRNYYIQWLNGSLIHGLWNLVFLFPNLSL  
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLTLLVLGMVWVASAIVDKNKANRESL  
YDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE  
AALTRRICNPTSCWLPIDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT  
GLSVLIVAIHILELLIDEAAMPQGTSLGQVSFSKLGSGFAVIQVVLIIFYLMVSSVVGFY  
SSPLFRSLRPRWHDAMTQIIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLGIFY  
IVFLYNAAFAGLTTLCLVKTFATAAVRAELIRAFGLDRLPLFVSGFPQASRKTQHQ

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**FIGURE 80**

GGCTGCCGAGGGAAGGCCCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGCGGNTTCNTCCCC  
GCTCGTCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC  
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA  
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC  
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG



**FIGURE 81**

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC  
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC  
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT  
CCCCGTTGTCNTCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA  
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT  
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC  
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC  
GCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT  
CCATCATCAGCAATGAGGTGCTGCACTCCC

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GATGATGCTCCTTGAGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT  
GGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCATGCTGCTGT  
GGGTGATATTACTGGTCTGGCTCCTGTCACTGGACAGTTTGC AAGGACACCCAGGCCCAT  
ATTTTCTCTCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTACTTGCAA  
GGGATTTCTGCTTCTACTCACCAAGAAAAAATGGTACCATTCGGTACCTTGCGAAAGAAA  
TACTAAGAGAAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG  
GCCAGGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTTCAGAGATGGGATTTCC  
TCATGCTGCCAGGCTAATGTTGAATCTCTGGGCTCAAGTGATCTGCTCACCTAGGCCTCTC  
AAAGCGCTGGGATTACAGCTTCGCTGATCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC  
TCTGTGGTTCTGAGGTGCCGGGCAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA  
TGATAATGTCTTGGCATTCTTAAATAAAGAACTGACTTCCAAAAA AAAAAAAAAAAAAAAA  
AAA

**FIGURE 83**

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL  
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEMGFPHAAQANVELLGSSDLLT

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**FIGURE 84**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT  
 GAGGCGGCCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGCGGAGGAGGCTGTGAG  
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACATGGCTCCGCAGAACTGAGCACCTTTT  
 GCCTGTGTGCTGTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTCTCTATAAGATCTTG  
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA  
 GCTTCATCCCGACCAGGAACCCCTGATGATCCACAAGCCAGGAGAAATTCAGGATCTGGGTG  
 CTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAA  
 GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTCACACTTCTTTGGGGATTT  
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA  
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT  
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTTGTCGGCAAGAGAT  
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT  
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG  
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG  
 AGATTACGGTTCGGAATCAAAGTTGTCAAGCACCCAAATATTTGAAAGGAGAGGAGATGATT  
 TGTACACAAATGTGACAACTCTATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT  
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT  
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA  
 TCACTTTTGATGTGGATTTTCCAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA  
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG  
 AATAAAATGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT  
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA  
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGAATGACC  
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCCTGAGT  
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA  
 GTTGTGTAGCAATTTCAATTCAAAATGCCAACTGGAGAAGTCTGTTTTTTAATACATTTTGTTG  
 TTATTTTTA

**FIGURE 85**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ  
AQEKFDLGAAYEVLSDSEKRKQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGT PRQQ  
DRNIPRGSIIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ  
MTQEVVDCPCPNVKLVNEERTLEVEIEPGVRDGM EYFFIGEGEPHVDGEPGDLRFRIKVVKH  
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHSRDKITRPGAKLWKKGEGLPNFD  
NNNIKGSIIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

**FIGURE 86**

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA  
GCGGCGGGCGGAGGAGGTTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT  
CCGCAGAACNTGAGCACNTTTTGCCGTGTTGNTGNTATACTTCATCGGGCGGTGATTGCCGG  
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG  
CCTATAGGAACTAGCCCTGCAGNTTTATCCCGACCGGAACCCCTGATGATCCACAAGCCCAG  
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA  
GTACGATAATTATGGTGAAGAAGGATTA AAAAGATGGTNATCAGAGCTCCCATGGAGACATTT  
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGAGGAACCCCTNGTCAGCAAGACAGA  
AATATTCCAAGAG

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**FIGURE 87**

GGCACGAGGCGGGCGGGCAGTCGCGGGATCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT  
 CTCTGCAGGTGTCTGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA  
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**  
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC  
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC  
 TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC  
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC  
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTACACTCTGAC  
 AGAGAAGCTTGTGGCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA  
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG  
 TACCTCCCGTTGGACCCAAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGACG  
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC  
 AGTCTCTGTGGCTGCTGAGGAGCATTGTGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG  
 CCAGATAAAGGCCTCCAGGCCCTGAAGGCTTCTGACAGGAGCAGTCTGCAATT**TAGT**GCCT  
 ACAGGCCAGCAGCTAGCCATGAAGGCCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCCTT  
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG  
 TAAAGCAGGAGATCCCCGTAGTTTATGCCTCTTTGTCAGTTGCAAACGTGGCTGGTGAGT  
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAAGAGGAGTATTGAAAA  
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTCAAGAAAAATTGAGCCACCGTCT  
 AAGAAATCAAGAGGTTTCACATTAAATTTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG  
 TGTGGCAATTCTGATCTGCATTTTCAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC  
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTATTGTATTATCTGCCT  
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGGTTTGGGTTTGAAGCTGAGGAAT  
 ACAAGTTGATGATTTCTTTTTATCTTTATGCCTGCAATTTACCTAGCTACCACTAGGTG  
 GATAGTAAATTTATACTTATGTTCCCTCAAAAAAAAAAAAAA

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**FIGURE 88**

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL  
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKSAS  
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLLSVSHLVLVTRNACHLTGGLDWI  
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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**FIGURE 89**

GCTTCATTTCTCCGACTCAGCTTCCACCCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCC  
CCACCACTGCAGCC**ATGAT**CTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA  
TTTGGAGTGTTTTCTGTTCCTTGGAAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT  
TGGAATGTTTTATTATTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAAGAACATTAGAT  
TCTTCTTCCAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGTATTGTAGTC  
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTGTTCAG  
GGGCTTCTTCTGTCTGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT  
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTA**TAA**CAACA  
AGTGAATTTGAAGACTCATTTAAAAATTTGTGTTATTATATAAAGTCATTTGAAGAATATTCA  
GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG  
CCTACAAAGTACCAGCAGCAAAATAGCAAAGAAGCAGTGAAACAGGCTTCTACTCAAGTGA  
ACTAAGAAGAGTCAGCAAGCAAACTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA  
ACTCTTGAAGGCTATTTGTGTTGTTTTTCACAATGTGCGAAACTCAGCCATCCTTAGAGAA  
CTGTGGTGCCTGTTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTGTCT  
TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA  
TGCATGAATTCGATTGGATTGTGTCAATTTAAAGTATTAAAAACCAAGAAACCCCAATTTTG  
ATGTATGGATTACTTTTTTTTGNCGNCAGGGCC

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**FIGURE 90**

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFQK  
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI  
RSFVDKVGESNNMV

**Important features:**

**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

**N-myristoylation sites.**

amino acids 11-16, 51-56 and 116-121

**Aminoacyl-transfer RNA synthetases class-II protein.**

amino acids 49-59

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCGACTCAGCTTCCC  
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGTGTCCCACCACTGCAGCCATGATCTCCTTAA  
CGGACACGCAGAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTCTCTGTTCTTTGGA  
ATGATCTCTTTTTTGACAAAGCACTACTGGCTATTGGAATGTTTTATTGTAGCCGGCTT  
GGCTTTTGTAAATGGTTTAGAAAGAACATTAGATCTCTTCTCCAAAACATAAAATGAAAG  
CTACAGGTTTTTTTCTGGGTGGTGATTTCAGTCCCTATTGGTTGGCCTTTGATAGGCATG  
ATCTCTCGAAATTTATGGATTTTTTCTCTTGTTC

**FIGURE 92**

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA  
 GGCTGCCAGGAAGGAGACGCCTTCTGAGTCCTGGATCTTTCTTCTCTCGGAAATCTTTGA  
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC  
 TGAAGTCTCAGTTTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGGCTCAGGGCTAATC  
 ATCAACACCATTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA  
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT  
 CGGGCACGGAATGCACCATCTTCACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAAT  
 GCCATCGTGGTTCTCAACCACAAGTTTGAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA  
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA  
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT  
 CGCAAGACGGTTGCCACCAAGTTTGACGACCTCCGGGACTACCCGAGAAGTATTTTTTCCT  
 GATTCACTGTGAGGGCACACGGTTACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC  
 GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC  
 ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTCAGAAA  
 TAATGAAATCCAACACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTGTATG  
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCCTGGCTGCAC  
 AAGCTCTACCAGGAGAAGGATGCCTTTGAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA  
 GACGCCCATGGTGCCCCCGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCTCGC  
 TGGTGCTCTACCCCTTCTTCCAGTTCTTGCTCAGCATGATCAGGAGCGGGTCTTCCCTGACG  
 CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT  
 GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAAACTGAATGACT  
CACTCAGGGAGGTGTCCACATCCGAAGGGAACCTTGGGGAAGTGGTGGCTCTGCATATCCT  
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA  
 CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGATGGGAGGAAGATGTTTTGTAATCTTT  
 TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC  
 TGTGTGGTGAAGTGTGAATTTGTTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG  
 GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTCATCCTTTGGTGTGAGTTTCTGT  
 AACCTTGGTTGCCAGAGATAAAGTGAAGTGCCTTTAGGTGAGATGACTAAATTATGCCTC  
 CAAGAAAAAAATTAAGTGCCTTTCTGGGTCAAAAAAAAAA

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MDLAGLLKSQFLCHLVFCYVFIIASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLV  
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLGGSKVLAKK  
ELAYVPIIGWMMWYFTEMVFCRSRKEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE  
ISMQVARAKGLPRLKHLLPRTKGFAITVRSRLNVVSAYVDCTLNFRNNENPTLLGVLNGKK  
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN  
WLFWASLVLYPFFQFLVSMIRSGSSLTASFILVFFVASVGVWRMIGVTEIDKGSAYGNSDS  
KOKLND

**FIGURE 94**

CTGAGCGCGGCGGTAGCATGAGGAGGAGAGTACGTCGCGCGGTGCTCTCGGGCTTTGTGCTCG  
 GCGCACTCGCTTTCCAGCACTCAACACGGACTCGGACACGGAAGGTTTCTTCTGGGGAA  
 GTAAAGGTGAAGCCAAAGAAGCAGATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA  
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG  
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT  
 TGGTACAAATTCGTCGTCATTTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA  
 AAACCTGCAAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAA  
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT  
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAAC  
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT  
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA  
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACT  
 AGTAAAGGATGTAACAGATTAACAGAGAAATTGAGAAAAGGAGAGGAGCAGATTCAGG  
 CAGCAAGAGAGAAGAATCCAAAAGACCCCTCAGGAGAACATTTTTCTTTGTGAGGCATTA  
 CGGACCTTTTTTCCAAATCTGAATTTCTTCATTATGTGTTATGTCTTTAAAAATAGACA  
 TGTTTCTAAAAGTAGCTGTAACATAACACCATCTCGATGTAGTAGACAATCTGACCTTAA  
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT  
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA  
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCC  
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA  
 TTTTGATCCTTTTAACTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAGCCAAACAT  
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTAC  
 CTGTTTGAGTAATACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC  
 ATCAGATGCTTTTATTCCAAACCTTTTTTTCACCTTTCCTAAGTTGTTGAGGGGAAGGCT  
 TACACAGACACATTTCTTAGAATTGGAAGAGTGAAGGAGGATGATTGAAGCTAGGAGTTAGAGACCAGCC  
 TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC  
 TGGGCACGTATTGAGACCATGTCTATTAATAAATAAATGGAAGCAAGAATAGCCTTAT  
 TTTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAATAATCTCCTTAAG  
 TGATACTTTTTTGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA  
 ATAAATTTGCAAAACATCATCTAAAAATTTAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 95**

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGVEVKGEAKNSITDSQMDDVEVVYTIIDIQ  
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH  
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPKGLFHRVPLVVANLGMSEQLGKTVSGSC  
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN  
RLKREIEKRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHSVSKSS  
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKKHALDLDDRWFKRSRLLDTDQDKRSKA  
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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**FIGURE 96**

GGCACAGCCGCGCGCGGGAGGAGAGTCCAGCCGAGCCGAGTCCAGCCGAGCAGCGGACAGCGCAGGGGACG  
 CCAAGCAGCGCGCAGCGAAGCGCCCGCGCGCCACACCCCTCTGCGGTCCCCGCGCGCCTGCCACCCCTCCCT  
 CCTTCCCCGCGTCCCCGCTTCGCGCGCCAGTCCAGTTGCGGGTTCGTGCCCCGCGAARCCCGAGTCCACCA  
 GCGCGCGCTCTGCTTCCCTGGGCGCGCGCGCCCTCCACGCCCTCTCTCCCTGGCCGCGCGCTGGCACC  
 GGGGACCGTGTGCTGAGCGCAGGCGCCAGCTCTACTTTTTCGCCCGGCTCTCTCGGCTGCTCGCTTCTCCAC  
 CACTCCCACTCCTTCTCCCTCCAGCTCCACTCGTAGTCCCGACTCCGCGACCGCTCGGCCGCTGCCGTAG  
 CGCGCTTCCGTGCGGTCCAAAGGTGGGACGCGTCCGCGCGCGCGCTGCTGGCTGCCGAGCTCACTCGAAAGTGTGCTCG  
 AAGTCGCGAGCTTTTACGTGTCCAAAGGCTTCAACAGAACGATGCCCCCTCCACGAGATCAACGCTGATCAT  
 TTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCTGCAAACTAAAGA  
 TGAATTTCAAAGTGTGTCAGCGAACAGTGAATCATTTGCAAGCTGTCTTTGCTTCACTTACAGAAAGTTTG  
 ATGAATTTCTCAAAGAACTACTTGAAGTGCAGAGAAATCCCTGAATGATATGTTTGAAGACATATGGCCAT  
 TTATACATGCAAAATTTGAGCTATTTAAAGATCTCTTCTGATAGATTGAACGTTTACTACGTTGGGAAATGT  
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGT  
 ACCACTTTACAGATGAGTATCTGGAATGTGAGCAAGTATACGAGGAGCTGAAGCCCTTCGGAGATGTCCCT  
 CGCAAAATGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGCTACTTTTCGTCAAGGCTTAGCGGTTGCGGG  
 AGATGTCGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCGAGTACCCATGCCCTGTTGAAGATGATCTACT  
 GCTCCCACTGCCGGGGTCTCGTGACTGTGAAGCCATGTTACAACACTACTGCTCAAACATCATGAGAGGCTGTTT  
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA  
 GGGTCTTTCAACATGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG  
 ATAATAGTGTCAAGTGTCTCAGAAGTTTCCAGGATGTGGACCCCAAGCCCTCCAGCTGGACGAAT  
 TCTCGTTCATCTCTGAAGTGCCTTCAGTGCTCGCTTCAGACCACTCACCCGAGGAGACGCCAACCCACAGC  
 AGCTGGCAGTAGTTTGGACGAGCTGGTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGTCTC  
 CCCTTGACACCAAGCTTTGCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGG  
 AAAGCCAAAGCAGTACCTGTTTGCATGACAGGAATGGATTAGCCAACAGGGCAACCAACCCAGAGTCCA  
 GCTTGCAGATCATCAGCAGTCCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGA  
 AGAATGCATCAATGGGACGAGTGGACTTCTTGATATCAGTGATGAAGTAGTGGGAAGGAGTGGAGT  
 GCCTGTGAGTATCAGCAGTCCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGA  
 GAAAGCCGACAGTGTGCTCGCTCCGCGCTGGGGCACAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTCTCTGG  
 TTATGCAGAGAGTGGAGATTAATTTCTCAACTCTGAGAAAAGTGTCTACAAAAGTTAAAAGSCACAGTT  
 ATCACTTTTCTACCTCTAGTGACTTTGCTTTTAAATGAATGGACAACATGTACAGTTTCTACTATGTGGC  
 CACTGGTTTCAAGAGTGTGACTTTGTTTCTCATCACTTTTGGAGGAAAGGGACTGTGCATGAGTTGAT  
 TCGTCTTCCGCAACCATGTTAAACGTGGCTAACAGTACAGTACAGAACTATAGTTAGTTGTGCAATTTGGT  
 TTTTATCACTCTATTATTGTTTGTATGTTTTTCTCATTTCTGTTTGGGGTTTTTTTTCACATGTGATG  
 CGCCTGTTTCTTACAAGCAACCCAGGTCCTTCTGGCACGTAACATGTACGTTTCTGAAATATTAATA  
 GCTGTACAGAAGCAGGTTTTATTATATCATGTTATCTTATTAAGAGAAAAGCCCAAAAGC



MARFGLPALCTLAVLSAALLAAELKSKSCSEVRRLVYSGFNKNAPLHEINGDHLKICPQ  
GSTCCSQEMEKEYSLQSKDDFKSVVSEQNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF  
VKTYGHLVMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRVNSQYHFTDEY  
LECVSKYTEQLKPFGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKSVVNPTAQCTHAL  
LKMIYCSHCRGLVTVKPCYNCSNIMRGCLANQGDLDFFWNNTDAMLMAERLEGPFNIES  
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGCPPKPLPAGRISRISSESASFARFRPHHPEE  
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLPNSVCNDERMAAGNGNEDDCWNGKGKSRYLE  
AVTGNGLANQGNNPEVQVDTSKPDILIRQIMALRVMTSKMKNAYNNGNDVDFDISDESSGE  
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**FIGURE 98**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT  
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA  
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC  
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCCAGAGGCCAC  
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA  
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTATGACAGTGTCTGGGCTGCCAAAGAAGC  
AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA  
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAACAATGTCAGCTAAGAAGCTT  
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA  
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCACTGTACCCACC  
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTGTTGCTCTC  
TCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT  
AATTACCTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTCAATTTAACCTTAAATGC  
AATCAGGAAAGTAGCAAACAGAAGTCAATAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

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MKVLISLLLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR  
KFMTVSGLPKKQCPDHFKNVKKTRHQRRHKPNKHSRACQQFLKQCQLRSFALPL

**FIGURE 100**

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT  
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA  
AAGCCAGACTTCCCCAAATTCCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA  
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA  
AACATTTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA  
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC  
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACC  
CTGACTGCATTTTGGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG  
ATGGAGAGGAAA

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**FIGURE 101**

MAVLVLRLTVVLGLLVFLTCYADDKPKDPDDSGKDPKPDFPKFLSLLGTEIIEHAVE  
FILRMSRSTGFMEFDDNEGKHSSK

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**FIGURE 102**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAGCCAGTGCCCCAGCGGAAGCACAGCT  
 CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTAC  
 CCTGCCCCCTGCACCTCATGGCTCTGCTGGGTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCC  
 CTTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG  
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG  
 CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC  
 CAAATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT  
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT  
 GGTGGTCTGCACTCTGGTGTGTGCTCTGTGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCC  
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA  
 AGCTGGGCCTTCATGTGCAGCAAGTTTTCGAGCCCACCTGGAACACATTGGGGATGGCTG  
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG  
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC  
 AAACAATCTTTCCAAGCTCCAAGGCACTCATTGTCTCTTCCCAGCCTCCAATTAGAACA  
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCT**TAG**CAGAATGAGAGAAGACATT  
 CATGTACCACCTACTAGTCCCTCTCTCCCAACCTCTGCCAGGCAATCTCTAATTCAATC  
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC  
 TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC  
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCATGCGT  
 CTCTAGGAACCTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT  
 CTCCCACCTACCACCTTCTTCTGAGCTGGGGGCACCAAGGAGAATCAGAGATGCTGGGGAT  
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTAAATAAATAGACGA  
 AACCACG

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MDILVPLLLQLLVLLLTLPPLHMLALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQI  
KGLTGASGKVALLELGCGETGANFQFYPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFV  
APGEDMRQLADGSMDDVVVCTLTCLCSVQSPRKVLQEVRRVLRPGGVLFWEHVAEYPGSWAF  
WQVFEPTWKHIGDCCCLTRETWKDLENAQFSEIQMERQFPPLKWLFPVGFHMGKAVKQSF  
SSQKCSFMSLQLEQATHQPIYLPRLGT

**FIGURE 104**

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG  
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA  
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG  
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG  
 TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAAA  
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG  
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACTCGCTCCAAT  
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATTCTCCGGTCTGGCTCAACAG  
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTAACTTTTGAAGGAA  
 AAGTAAAGGAGGATCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC  
 TTGCCAATTCTGGTTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA  
 AGGTGATATCTTGGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG  
 AAGATTGTGATTAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTAC  
 ATTGCTATCTTGACTATAAAAAGGAAAGAAATTCGTAAGCTTTCCATGAAAGCCAGCACCTG  
 CTCATTTAATCCTGGAGTTTTTGTGTGCAAACTGACGGAATGGAACGACAGAATATACTA  
 ACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT  
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC  
 TATGTGGAATGTCCGCCACCTTGGTTCAGTGCTGGAAAACGATATTCACCTCAGTTGTAA  
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT  
 ACTGATGTTTGGGAAAAATGTTATATCCAGACCCAACAGGCAAATTCACCTAATCCGAAG  
 ATATACCGAGATCTCAAACATAAAGTGAACAGAAATTTGAACTGTAAGCAAGCATTCTCAG  
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA  
 GCAAGCCATGAAAAAGATGTGTCAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC  
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT  
 ACTACAAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA  
 TAATTCAAACCTGCTGTTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAAATAAACTT  
 ACATTTTTT





**FIGURE 106**

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT  
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT  
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT  
TGCAGCTATAAACAGCATTTCAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC  
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA  
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA  
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCAGCG  
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTAC  
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTTCAGCCTCTAC  
TAAAGTTGTCATCCGTGGAGCAGGAAA

**FIGURE 107**

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG  
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC  
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTTCGGGGCGCGGGCTGCA  
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGGCGGGCGAGCCTTTGAGGGGAACGACT  
 TGTGCGAGCCCTAACCCAGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT  
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT  
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC  
 CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGGAATTGTAG  
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA  
 GGAGATTCTGTGGTCATCGTGCATCTGAAGACAGGCTTGGGGGGCCATTGCAGCTATAA  
 ACAGCATTACGACACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA  
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG  
 TCAATTTTGACCCATAAATTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGAATCC  
 ATGAACCTTTAACCTTTGCAAGGTTCTACTTGCCAAATCTGGGTTCCAGCGCAAGAAGG  
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTACAATACAGCA  
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT  
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA  
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC  
 CTGACGGAATGGAACGACAGAATATACTAACCACCTGGAATAATGGATGAAACTCAATGT  
 AGAAGAGGGACTGTATAGCAGAACCCCTGGCTGGTAGCATACAACACCTCCTCTGCTTATCG  
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT  
 GCTGGAATAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA  
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATCCA  
 GACCAACAGGCAAAATCAACCTAATCCGAAGATATACCGAGATCTCAACATATAAGTGAAA  
 CAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG  
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGAGCTAG  
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT  
 ATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA  
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT  
 GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTTCAATAGGTAAAAAAGAAAAA  
 AAAAAA

CTGACAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT  
GAAGGCCGGCCATACCAGAGTCTCGCTCGGCATGGGCCCTCACCATTGAGGCAGTCCACTG  
TCTGTGCTGGTCTGAGGGTGCTGCCGTGTCATGGGGGCAGCCATCTCCAGGGGGCCCTCATC  
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTGTGCTGCTGCTCTGGGTCACTCTGTGCTG  
GGCCTGCCATTCTCGTCTGCCGAGTTGACTCTCTCTGAAATCCAGTCCCAACTCCAGCCC  
TGGCCCTGTCTGAGAAGGCCCCACCACCCAGAAGCCAGCCATGAAGGCAGCTACCTGC  
TGCAGCCCTGAAGGCCCTTGGCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG  
CCTGGAATTAGGATCCCAGAGTTAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT  
TGGAGCTGGACCCAGCGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC  
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT  
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTTTCCCTAGGCTGAGCAC  
CTAGGCCCTCTAGGTTGGGAAGCAAATGGAACCCATGGCAATAATAGGAGGGTGTCAG  
GCTGGGCCCTCCCTGGTCTCCAGTGTTTGCTGGATAATAAATGGAATATGGCTCTAA  
AAAAAAAAAAAAAAAAAA

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**FIGURE 109**

MGAATISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH  
PRSPAMKAATCCSPEGPWPSLEPRT

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**FIGURE 110**

GTTTGAATTCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA  
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA  
 CTCCCTATTTGCATCTGTTTTGTATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAA  
 TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC  
 ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT  
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC  
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA  
 TCCACAGGCATCACGGCAGTGTCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT  
 GACAGTTGAGCTTTTCCAAATCACAAATAAGCCATCAGCAGTGTCCCTTCTGCTGTTCC  
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTCTGGGTCTCTGGGTGGCTGTGCTGCTG  
 AGCCTGGGAACTGCAGGAGCTGCCAGGTATGGAAGGCGGCCAAGTGAATATAAGCCCCCT  
 TTCGGGCATTTCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATCA  
 TCCTTGCGTGCCAGCAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCACAGAAGT  
 AAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTACCATCA  
 AGGAACCGTTGTGAAAGGTCATTTTTAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCA  
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGTACCTGTTCCGA  
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA  
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT  
 TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGGAGACTTCATAATTTTTCTA  
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG  
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGCCC  
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCATTTTCTGTGTTTTGCTGTTGAT  
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT  
 CGTAAAAAGGAGCAACAAATTAACCAATGAAGGACACAGCAGGACAAGCACTCATTAAAGGA  
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGATTAGATATCCCATTTAGGTATCTGTACCT  
 GGAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT  
 AGTGAATTTTTTTTTAAAGACCTAATAAACCCATTCTCTCTCAAAA

**FIGURE 111**

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYDTNDL  
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ  
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI  
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQCTVVKGSFLISVVRIPRIIVM  
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL  
SKNSSHFTSINCFGDFIIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH  
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN  
EEGTELQAIVR

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**FIGURE 112**

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTT  
 AGAAATTAATTTGTATGGGATTTGTGATGCAAGGAAGCCTAAGGGGAAAAAGAAATATTCATTCTG  
 TCTGGTGAAAATTTTTTGAAAAAAAATTTGCCCTTCTTCAAACAAGGGTGTCATTCTGATATT  
**TATG**AGGACPTGTTGTTCTCAGTATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTTGCCTGG  
 TGACTGGAGTACATTCAAACAAAGAAACGGCAAAGAAGATTAAAAGGCCCAAGTTCACTGTG  
 CCTCAGATCAACTGCGGATGTCAAAGCCGGAAGATCATCGATCCTGAGTTTCATTTGTGAAATG  
 CCCAGCAGGATGCGCAAGACCCCAAATACCATGTTTATGGCATGACCTGTATGCTATCCTACT  
 CCAGTGTGTGTGGCGCTGGCGGTACACAGTGGTGTGCTTGATAATTACAGAGGGGAAAATACTT  
 GTTCGGAAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCACCGGTGTCGAATCGTT  
 ATCCCTACGACGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAAC  
 CCTACCCATCAGCTCTTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGGTGAGACC  
 ACAAAAAGCCTATCAGAGGCCACTTATCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA  
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCCAAGGCCATCCCTTCTG  
 CTGCTTCTACCAACAGCATCCCCAGACCACAATCAGTGGGGCCACAGGAGCCAGGAGATGGAT  
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAACAGGCCCAGAGCTGATCCAGGTATCCA  
 AAGGCCAGATCCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGCGGATGTCAGCCTGGGAC  
 TTGTTCCAAAGAAGAAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC  
 TGCAAAATTGACTTGTCTGTTTAAATTGATGGGAGCACCAGCATTTGGCAACAGGCCGATCCG  
 AATCCGAAGCAGCTCTGGCTGATGTTGCCAAGCTCTTGACATTTGGCCCTGCCGCTCCAG  
 TGATGGTGTGTTCTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACACACAG  
 AATTTCTGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT  
 AGGCTCGGGCATCTCCTTTGTGACCAGAATCTTTTCCAAAGCCAATGGAACAGAAAGGG  
 GGGCTCCCAATGTGGTGGTGGTGGATGGTGGATGGCTGGCCCAAGGCAAAAGTGGAGAGGGT  
 TCAAGACTTGCAGAGAGTCAGGAATCAACATTTCTTTCATCACCATTGAAGTGTGCTGA  
 AAATGAGAAGCAGTGTGTTGGTGGAGCCCACTTTGCAACAAAGGCCGTGTGCAGAACAAAGC  
 GCTTCTACTCGCTCCAGTGCAGAGCTGGTTTGGCCCTCCCAAGACCTGCAAGCTCTGTTG  
 AAGCGGCTCTGGCAGACTGACCGCTGGCCCTGCAGCAAGACCTGCTTGAACCTGGCTGACAT  
 TGGCTTCTGTCATCGACGGCTCCAGCAGTGTGGGGACGGGCACTTCCGACCGCTCCTCCAGT  
 TTGTGACAACTCACCAAAGAGTTTGAGATTTCCGACACGGACACGGCATCGGGGGCTGTG  
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTCGACAAGTACAGCAGCAAGCCTGACAT  
 CCTCAAGCCCATCAAGAGGCTGGGCTACTGGAGTGGTGGCAGCAGCAGCGGGGCTGCCATCA  
 ACTTTCGCCCTTGGAGCAGCTCTTCAAGAAGTCCAAGGCCCAACAAAGAGGAAGTTAATGATCCTC  
 ATCACCAGCGGAGGTCCTACGACGACGTCGGATCCAGCCATGGCTGCCATCTGAAGGG  
 AGTGTATCACCATTGCGATAGGCGTTGCCCTGGGCTGCCCAAGAGGAGCTAGAAGCTATTGCCA  
 CTGACCCCCGCCAGAGACACTCCTTCTTTGTGGACGAGTTTGACAACTCATCAGTATGTC  
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTACAGAG  
 CAGGCAGAGCACAGCAAGTGCTGCTTTACTAACTGACGTGTGGACACCCCAACCGCTTAA  
 TGGGGCAGCAGCGTGCATCAAGTCTTGGGCAGGGCATGGAGAAACAAATGTCTTGTATTATTA  
 TTCTTTGCCATFACCTTTTTCATATTCAAAACCTTGGAGTTACAAAGATGATCACAAACGT  
 ATGAAATTGAGCCAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGAACATTT  
 GTCTTAACAAATAATGTTCCGAAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT  
 GTGAGATTTTAAAGTTGTTATTTCTGATTTGAACCTCTGTAAACCTCAGCAAGTTTCAATTTT  
 GTCATGACAATTGAGGAATTTGCTGAATTAATGTTTGAAGGATGAAAAATAAAAAATAAAAA  
 AA  
 AA



MRTVLTMTKASVIEMLVLLVLTGVHSNKETAKKIKRPKFTVPQINCVDKAGKIIDPEFIVKC  
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKAVAGQSGYKGSYNSGVQSL  
SLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAGAGETTKAYQRPPIPGTTAQPVTLMQ  
LLAVTVAVATPTTLPRPSPSAASTTISIPRQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ  
RQDPGSAAFQKPGVADVSLGLVPKEELSTQSLPEVSLGDPNCKIDL SFLIDGSTSIGKRFR  
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTSNRDLKTAIEKITQRGGLSNV  
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE  
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRKVCDTRLACSKCTCLNSADI  
GFVIDSSSVGTGNFRTVLQFVTNLTKFEIKSLDTRIGAVQYTYEQRYLEFDKYSKPDII  
LNAIKRGVYWSGSTGAAINFALEQLFKKSKPNRKLMLILTDGRSYDDVRI PAMAHLKG  
VITYAIGVAAWAAEQEELEVIATHPARDHSFFVDEFDNLHQYVPRI IQNICTEFNSQPRN

**FIGURE 114**

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA  
TGCCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT  
 GCGCCAGGTCCCAGCGGCTCCGCGCCAGATCCCGCCCACTACAGTTTTTCTCTGACTCTAAT  
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATCCAAGAGTGGTTGAAG  
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGAACAACATT  
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA  
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCCGAAAACCTC  
 TCCCAGCCTTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG  
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC  
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCAAGATGTGGCCAGAGTGGCTTTGATGC  
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC  
 AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCTACTTTGAGTACTTGGT  
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAAG  
 CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAGATGTACAAGGGGACT  
 GTGTCCATGCCAGTCTTCCAGTCCTTGGAGGCCCTACTGGCCTGGTCTTCAGAGCCTCATTGG  
 AGACATTGACAATGCCATGAGGACCTTCTCACTACTACACTGTATGGAAGCAGTTTGGGG  
 GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA  
 CTTCCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCT  
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGGCGAT  
 TTGCAACAATCAAAGATCTGCCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTCTCTG  
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCACTTCATCCACAACAATGG  
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGTACA  
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG  
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC  
 GAAATTTTCAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC  
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAACAAGAGGTCCTCA  
 CTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT  
 AGACTCCTCATTAACCACTGGATAATTTTTTATTTTTATTTTTTGGGCTAAACTATAATA  
 AATTGCTTTTGGCTATCATAAAA

**FIGURE 115**

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE  
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL  
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM  
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK  
AIRNYTRFDDWYLVWQMYKGTVSMVPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG  
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPPTLLELGRDAVESIEKISKVECG  
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY  
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT  
LFSPENHDQARERKPAKQKVPLLSCPSPFTSKLALLGQVFLDSS

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AAGGTTACATTTTCTTGGAACTCTCTAGGCCACTCCTGCTGATGCAACATCTGGGTTTG  
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA  
 ATTCAGGCTTCGTCGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACATGTTCTAGGTCAAACCTGAGTCTACCA  
**AATG**CAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
 ACGCATTGATTCCATGTTTGGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACTC  
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA  
 AACAGTGTACTATTCTGTCGAATACAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
 GGATCCCCAGCAGCTGCTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC  
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
 GAGCATCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCGAGTTGAGTTT  
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGATGG  
 GGGTATTCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATCTGTGTGAAGGCCGACA  
 CATTCTGTGAAGGCCATTGGGAGGTACAGCGCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
 GGAGAGGCCATTCCCTGGTATCGGCCCTGTGTCCTTTGTTGGCTTCATGCTGATCCTGTG  
 GGTCTGTGCCACTGTTCTGTGGAATAAGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG  
 TGGTCTCTCCAGACACCTTGAAATAAACCAATTCACCCAGAAGTTAATCAGCTGCAGAAGG  
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT  
 CTCAT**TAG**GTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC  
 ATGAGGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTGTCTAACAGAACC  
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC  
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA  
 TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG  
 TGTTTCTGGAGAGCAGGACATAATGTATGATGAGAATGATCAAGGACTCTACACTGGGT  
 GGCTTGGAGAGCCACTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
 TGTGAGTTCACTTCAAGCCCATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGTGAATGTATGT  
 GTGCAATCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTCT  
 TGTTGGTAAAGTACAGAATTACGCAATAAAAAGGGCCACCTTGGCCAAAAGCGGTAAAAAA  
 AAAAAAAAAA

**FIGURE 117**

MQTFTMVLEEIWTSLFMWFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLWMWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDDTDDITATVPYNLRVRATLGSQTS  
SILKHPFNRRNSTILTRPGMEITKDGHLVIELEDLGPQFEFLVAYWRRREPAAEEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPLVLALFAFVGFMILILV  
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation sites.**

amino acids 40-43 and 134-137

**Tissue factor proteins homology.**

amino acids 92-119

**Integrins alpha chain protein homology.**

amino acids 232-262

**FIGURE 118**

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACCTGATGACATCAGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAGAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGC GGCGCAAGGG  
GTTNGCGAACCCCTTGC GGCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC  
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

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CGGACGCGTGGGCGCCACCTCCGGAACAAGCAATGCTGGCGGCACGGTGGCAGCGCGGTG  
GCTGCTCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG  
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG  
AATGTGGCAGCGAGTGC GGCTTCACAGACCAGACTACCGAGCCCTGCAGCAGCTGCAGCG  
AGACTTGGGCCCCACCACTTTAACTGTCTCGCTTCCCTTCAACCAAGTTTGGCCAACAGG  
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGACCTACAGTGTCTATTCCCC  
ATGTTTAGCAAGATTGCAGTACCCGCTACTGGTGCCCATCTGCCTTCAAGTACCTGGCCCA  
GACTTCTGGGAAGGAGCCCACTGGAACCTCTGGAAGTACCTAGTCCCGCAGTGGAAAGG  
TGGTAGGGCTTGGGACCACTGTGTCTAGTGAGGAGGTAGACCCCGATCAGCAAGCGCTC  
GTGAGGAAGCTCATCTCTACTGAAGCGAGAAGACTTA~~TA~~CCACCGCGCTCTCTCTCCACCA  
CCTCATCCGCGCCACTGTGTGGGGTGACCAATGCAAACTCAAATGGTGTCTCAAAGGGAG  
AGACCCACTGACTCTCTCTCTTTACTCTTATGCCATTGGTCCCATATTCTTGTGGGGGAA  
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCTGGCCAATGAG  
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAATGTGTGGCAAA  
TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC  
CTCATAGGGCTGTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCTTAGGCAGTGCCAGC  
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTATTCAAT  
AAAAACTTGCATCCAACATGAATTTCCAGCCGATAGATAATCCAGGCCAAAGGTTTAGTTGTT  
GTTATTTCTCGTATATTATTTCTTCTATTACAAAGAAATGCAAGTTCAATGTAACAATCCA  
ACAATACTCTCAGTATATAAAATAAAAAAAGAAAGTATCTCTCTCAAAA

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**FIGURE 120**

MVAATVAAAALLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ  
HYRALQQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG  
AHPAFKYLAQTSKGKEPTWNFWKYLVPDGVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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CGGACGCGTGGGCGGGCGGGACGCAGGGCAAAGCGAGGCC**ATG**GCCTGTCTACGTCGGGATGCTGCCTCTGGGAGAGGCTGTGCGCCGGGAGCTCGGGGGTCTCTGGGGGCCCGGGCCCTCTCTCGGATGTGGCAGGACGAGGTCGTGAGGTTGCTCGCTTCTCAGTTCCAGAGAGGTGGATCGCATGGTGTCCACGCCCATCGGAGGCCCTCAGCTACGTTTCAGGGGTGCACCAAAAAGCATCTTACACGACAGCTGTGGGCGAGTGCCTCGGAGACACAGCAGAGGGTCCCGAAGACGAGAGGCCCTTGTGCTCGCTCTCATGAAGACCTCAGGTTGACCTTGGCCCACTAAGGAGAGGTGGACAAAGCTGTCTTGGCCTCTGAGCATTTGGCCTCTGCAAAAGGTGACCGGCTGGGCATGTGGGGACTAACTCTATGATGGGTGCTCATCGAGTTGGCCACCGCCAGCGGGGCATCTTCTGGTGTCTGTGAACCCAGCTACAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAAGGCCCTTGTGTTCCCCAAGCAATTCAAAGCCCCAGCAATACTACAAGCTCTCTGAAGCAGATCTGTCCAGAAGTGGAGAATGCCACGCCAGGGCCCTGAAGACTCAGAGCTCCGAGTCTGACCATACGTCATCTCGGTGGATGCCCTTTGCGGGGGACCGTGTCTCTGGATGAAGTGGTGGCGGCTGGCAGCACACGCGCAGCATCTGGACAGGCTCCAATAACACAGCAGTTCTGTCTGCTGCATACCCCATCAACATTCAGATTCACTTCGGGGACACAGGCGAGCCCAAGGGGGCCACCCCTCTCCCACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCCTGAAACTCGGATCGAGAAGACACGAGCAGTGTGGGATGTATCTGCCAACCCCTGTACCATTTGCCTGGTTCGGTGGCAGGCACATGATGTGTCTGATGTACGTGTGCACCCCTCATCTGGCCTTCCCATCTTCAATGGCAAGAAGGCCTGGAGGCCATCAGCAGAGAGTGGACCTTCTGTGATGGTACCCACAGATGTTCTGGTGACATCTGCAACAGCCAGACTTCTCAGACTTATGACATCTGCAGATCTGTGGGAGTGTGATCTGCTGGTGGTCCCTGCACCTTCAGAGTTGATCCGAGGCATCATCAACAAGATAAATATGAAGGACCTGGTGGTGCCTTATGGAACCAAGACAGCTCCGTGACATCTCGGCACCTTCCCTGAGGACACTGTGGAGCAGGAGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGTCATCCGAGGTAAGTCTGCTGATGCTGGGCTATCGGGTGAGCCTCAGAAGACAGAGGAAGCAGGGATCGGATGGGGGAAGAGATTTGTGCTGCAATCTCGGTCAGAGCGGGGAGGAGACCAGGTGGAGGAGATAAAAGCTTTCTGCAAAAGGGAGATCTCTCACTTCAAGATTCGAAGTACATCTGTGTTGTCAACAACATCCCCCTCACCATTTCAGGAAATTCAGAATAATCAAACTTCAAGTTCAGAGTCAGATGGAAACGACACTTAAATCTG**TGA**ATAAAGCAGGCGCTGTCTTGGCCGGTTGGCTTGACTCTCTCTGTGAGAATGCAACCTGGCTTTATGACCTAGATGTCCCCGACCCAGCTTCAGAGCCAGCCGATCAAAATGTCAAGAAATTCAGGATTCAGGACCACTGAAGGCTCTGGATGGGTTCGGGAACTCGCCTGGGCACAAGGTGCCAAAAGCAGGCAGCCTGCCACGGCCCTCCCTCTCTGTGATCCCCACATTTCCCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTTGAAAAAATAAAAAA

**FIGURE 122**

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFSSREVD RMVSTPIGGLSYVQ  
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG  
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPPKQFKTQQY  
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLP GTLLLDEVVAAGSTRQHLDQLQYN  
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY  
HCLGSVAGTMCMY GATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY  
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVA YGTTENS PVTFAHFPEDTVEQKAESVG  
RIMPHTEARIMMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT  
MNEQGFC KIVGRSKDMIIRGGENIYPAELEDFFH THPKVQEVQVGVKDDRMGEEICACIRL  
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domains:**

amino acids 140-161, 213-229, 312-334

**Putative AMP-binding Domain Signature:**

amino acids 260-271

**N-myristoylation Sites:**

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,  
314-319, 318-323, 379-384, 380-385, 409-413

**N-glycosylation Site:**

amino acids 282-285

**FIGURE 123**

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA  
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTCCGTGGCAGGCACAATGATGTGTCTG  
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC  
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA  
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC  
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT  
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTGCGGCACCTCCCTGAGGACACTGTGG  
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG  
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT  
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT  
ATTGGACAGGAGATGTCGCCAC

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### FIGURE 124

GAGCAGGACGGAGGCC**ATG**GACCCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC  
AGGCTGGCTGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG  
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCGCCGGGC  
GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC  
AGTGC GGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCTGGATCTTCACGGG  
TTCTGGCGTTCA**T**CCAGCTGCAGCAATGCCTCAGGATCGCTGCAACGCCAAGCTCAACCTC  
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGCTGGAGTG  
CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGTTACATCGCGCCGGTCTGTAGCT  
GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA  
GCTAATGTGACTGTGCTCTTGCCTTTCGGGCTGTGTCCAGGATGAATTCTGCATCGGGA  
TGGAGTAACAGGCCCAAGGTTACGCTTACGTTGCTGGCTCTGTTGCCAGGGGTCGGCTGTA**A**CT  
CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCGGGCTGCCCCCT  
CCAGAGCCCAAGCATGTGGCCTCAACCACATCTGTCA**C**CACTTCTACCTCGGCCCCAGTGAG  
ACCCACATCCACCACCA**AA**CCCATGCCAGCGCCAACCAAGTCAGACTCCGAGACAGGGAGTAG  
AACACGAGGCCTCCCGGATGAGGAGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC  
CGCAGCAATT**C**AGGGCAGTATCTTGCAAAGGGGGCCCCAGCAGCCCCATAATAAAGGCTG  
TGTGGCTCCCA**C**AGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTG**T**  
**G**AGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT  
CATACTTCTCTGTTCCCA**C**CACTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTCCC  
CAGTATCCCAGCTTCTGCTCGGCTGGTTTGGCGCTTTGGGAAATAAAATACCGTTGTATAT  
ATTCTGCCAGGGGTGTTCTAGCTTTTGAGGACAGCTCCTGTATCTTCTCATCCTTGTCTC  
TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG  
AGAGAGAGGATGCTAAGCTTCTACTCACTTCTCTAGCCAGCCTGGACTTTGGAGCGTGG  
GGTGGGTGGGACAATGGCTCCCCTACTTAAGCACTGCCTCCCTACTCCCGCATCTTGGG  
GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCAGGGGGGGGCCCGTAC  
CCAATTGCGCCCTATAGTGAGTCGTA

**FIGURE 125**

MDPARKAGAQAMIWTAGWLLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT  
EAVGAVETIHGQFSLAVRGCGSLPGKNDRGLDLHGLLAFIQLQQCAQDRCAKLNLTSRAL  
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGC'DGNVTLTAANVT  
SLPVRGCVQDEFCTR DGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRI PPLVRLPPPEPTT  
VASTTSVTTSTSAPVRETSTTKPMPAPTSQT PRQGEHEASRDEEPRLTGGAAGHQDRSMSG  
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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CGGGACTCGGCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT  
TGGTGCTGGTCTTCTCTGCAAGCTGTGTGCCCCCATGGTCTTGCCAGTGCAGCTGAAAAG  
GAGAAGGAAATGGACCCCTTTTCATTATGATTACCAGACCTGAGGATTGGGGACTGTGTGT  
CGCTGTGGTCTCTCTCGTTGGGATCCTCCTTATCTTAAGTCGCAGGTGCAAGTGCAGTT  
TCAATCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCAGGTGGAGAACCTCATACCGCC  
AATGCAACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGTGGGAAGCCTCTGGAA  
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAAATGTCGATGCT**TAA**GAAAACCGGCCACTTC  
AGCAACAGCCCTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCATATCCCTCTA  
ACACCATTCTCCACCTGATGATGCAACTAACACTTGCTCCCCACTGCAGCTGCGGTCTC  
GCCCACCTCCCGTGATGT  
GTCTTTGTGGCTACTTGTTTGTGGATGGTATTGTGTTTGTGTAGTGAATGTGACTCGCTTT  
CCCAGGCAGGGGCTGAGCCACATGGCCATCTGCTCCCTGCCCGTGGCCCTCCATFAC  
CTTCTGCTCTAGGAGCGGTGCTTTGTGCCCGAGACCCAGCCCCCTCCCTGATTTAGGGATGC  
TAGGGTAAAGAGCAGGCGCAGTGGTCTTCAGTCTCTTGGGACCTGGGAAGGTTTGCAGCAG  
TTTGTGCATATTCTTCATGGACTCCTTCTACTCCTTTAACAAAAACCTTGCTTCTTATCCC  
ACCTGATCCAGCTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCC  
CAGCGTTGACGTGAGGCAGGCTATGCCCCCTCCGTGGTTAATTTCTCCAGGGGCTTCCAG  
AGGAGTCCCCATCTGCCCCGCCCTTACAGAGCGCCCGGGGATTCCAGGCCAGGGCTTCT  
ACTCTGCCCTGGGGAAATGTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG  
GACCCCTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCAGCTCATCCAG  
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTC  
GTTGGGGCCAGCACACCGGATGGATGGAGGGAGAGCAGAGGCCTTTGCTTCTCTGCCTACG  
TCCCCCTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTGCGCTGTCCGTTGCTGAGA  
GCGGTGAGCGAGGTGGTTGGAGACTCAGCAGCTCCGTGACGCCCTGGGAACAGTGCAGAG  
GTTGAAGGTCTAAACGAGAGTGGGAATCAACCCAGATCCCGCCCCCTGCTGTCTGTGTGT  
CCCGCGGAAACCAACCAACCGTGCCTGTGACCATTGCTGTCTCTGTATCGTGATCTAT  
CCTCAACAACAACAGAAAAAAGGAATAAAATATCCTTTGTTTCCT

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**FIGURE 127**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK  
CSFNQKPAPGDEEAQVENLITANATEPQKQRTVQPSGGSLWNLRRLLEPLDANVDA

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**FIGURE 128**

AAACTTGACGCCCATGAAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT  
CCACTCTGCCCAGGGAGCCACCCCTGGGTGGTCCTGAGGAAGAAAGCACCAT TGAGAATTATG  
CGTCACGACCCGAGGCCTTTAACACCCCGTTCTGAACATCGACAAATTGCGATCTGCGTTT  
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT  
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT  
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT  
CTTTCCTGCCTCAGGAACCTCAATAAAACATTTTCATCCAAA

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**FIGURE 129**

MKIPVLPAVVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKADE  
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

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**FIGURE 130**

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCC**ATG**GGGGTGGAGATTGC  
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTC  
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGCCATGGGAGATCTCTCCTGTGGC  
TTTGCCGGCCACTCA**TGA**GAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT  
TCATGATTTAATAACCATCCCTTTCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA  
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCTTTATTTTT  
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC  
TTCACTATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT  
TATCCCTGGGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA  
TGTTATTCTAATATTAGTACATTCAGTTGTGATGAATATGAATAACCAGAATCTATTTCTT  
AAAAGTTTTGAGTATATTTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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**FIGURE 131**

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

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**FIGURE 132**

GGGGAATCTGCAGTAGGTCGCCGGCGATGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG  
 GCTGCTGTTGTTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGA  
 AAGTATTTATTGACCAAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAGTCAAAC  
 TGCAGCTGCTACCATGGTGTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG  
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA  
 GACTGTACCGGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT  
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA  
 GGTTCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC  
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGCCAATTTAT  
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG  
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG  
 ATCCTCTCATCTTCTGTCTCGGAAAAACCCAAAACCTTGTGTATGCAGAATACACAAAAAC  
 CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT  
 GGATCACTGCAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA  
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATCTTTC  
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA  
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA  
 GCCAGTTTATTAGGAACCAATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG  
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAGGTTATGATCAAATTAT  
 TCCCAAAATGTTGAAACTGAACTATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCA  
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA  
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCAGAGCAACTCTTGAGA  
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA  
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCATTTTCTTAAGACCAATC  
 ACAGCTTGTGCCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA  
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA  
 CTCATTGCTGGAATTGTGAAATTATTCAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG  
 AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG  
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAAACCATAAATCTGTACTCAG  
 GAGGTTTCTATAATGCCACATAGAAGAGGCCAATTGCATGAGTAATTATGCAATTGGATT  
 TCAGGTTCCCTTTTTGTGCCCTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

**FIGURE 133**

MEWWASSPLRLWLLLFLLLPSAQGRQKESGSKWKVFIDQINRSLENYEPSSQNCSCYHGVIE  
EDLTFPRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD  
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPYPTGLGRWDL  
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT  
LGKPAAKDVHLVDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH  
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQDDITCYWENLLSEYSKFLSY  
NVTRRKGYDQIIPKMLKTEL

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**FIGURE 134**

CACCCCTCCATTCTCGCCATGGCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT  
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCTGTGCGCTTTACCTCCCCTTCGCCCACTTCTT  
 GGAGGATCCCGAGTCTGGTGGTCCGGATGCCCGCCAGGATGGCTGGCTGCCCTGCAGGA  
 CCGCAGCATCCTTGCCCCCTTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC  
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTTCAG  
 AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGACGTGGTGATGCGGTACTGGGAGCC  
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC  
 TCCTCTGCTTTGTGCTCCATGTCTCTCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT  
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC  
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG  
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCCTACCCCTGGGCACGGACCGTCTCCTCCTTGCT  
 TTCTCCTTACCCTCTACCTGGGCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT  
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCAAGGATGGGGAGGCAGAGT  
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC  
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT  
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCATAAATTCTGAGTTTCAGCCA  
 CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC  
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC  
 CTGACCACTCCCCCTGGCACTGTTACTTGCCCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT  
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTC AACGGTCATAGCTGTCCCTCCA  
 GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT  
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC  
 CTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

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**FIGURE 135**

MAPALLI PAALASFLAFTGVEFVRFTSLRPLGGI PESGGFDAQGWLAALQDRSILAP  
LAWDLGLLLLFVQGHSLMAAERVKAWTSRYFGVLQRSIYVACTALALQLVMRYWEPIPKGPV  
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGKQVYYHVLGLGEPLALKSP  
RALRLFSLRHVPCVELLTVLWVVPTLGTDRLLLAFLTLTYLGLAHLSDQDLRYLRAQLQR  
KLHLRSRDPGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

**FIGURE 136**

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA  
 AGAAATTGCCAAACCATGTCTTTTTTTCTGTTTTTCAGAGTAGTTTCACAACAGATCTGAGTGT  
 TTTAATTAAAGCATGGAATACAGAAAACACAAAAAACTTAAGCTTTAATTTTCATCTGGAATT  
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA  
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG  
 AGCTGCTGTGGATGCGCTCGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC  
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTCTTTGTGATGTGGTACCTCAGCCT  
 TCCCCACTACAATGTGATAGAACGCGTGAACCTGGATGACTTCTATGAGTATGAGCCGATTT  
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT  
 CTGGTCATTCTGGTGACCTCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC  
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG  
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCCTTAGAGGATGAACACCTTCTTTATGGT  
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATATGGC  
 ATTCAGGTGGGTAAGTGAATTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG  
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTAAACCTAAACCACTCAGAGAAGTTT  
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAACCCATAT  
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAA  
 TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTCACGTAAAACCCATCAAGTTT  
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTTATAAAGTGAACATTATATCCAGAAGA  
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG  
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACC  
 ACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA  
 GTGTTAAATAAAGTAGGTACTGTGGAATAATCATGGGAGGTGAGTGTGCTGGCTTACACTG  
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTACACTTGTGATTATTAGTC  
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGTCTAAA  
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG  
 TGTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACATGTAGAGTTTTATTATTG  
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA  
 TGTAGTTCTGTGTCAAAAACCTTCTTCACTGAAGTTATACGTAACAAAATTTTACCTGTTTT  
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA  
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT  
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC  
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAAT  
 ATTTTACTGTGGTAATATAGAGAAGAATTAAGCAAGAAAACTGAAAA



**FIGURE 137**

MASALWTVLP SRMSLRSLKWSLLLLSLLSFVMMWYLSLPHYNVIERVNW MYFYEYEP IYRQD  
FHFTLREHSNC SHQNPFLVILVT SHPSDVKARQAIRVTWGEKKS WGYEVLTFLLGQEA EK  
EDKMLALSLEDEHLLYGD IIRQDFLD TYNNTLKT IMAFRWVTEFCPNAKYVMKTD TDVFIN  
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPF PYCSGLGYIMSRD  
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVN IHIPEDTNLF FLYRIHLDVCQLRRVIAAHG  
FSSKEIITFWQVMLRNTTCHY

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CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT  
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA  
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA  
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAATGGCTTTGCTGCAACC  
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT  
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC  
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAGTCGATGACCTGAGCAAGTTCGGA  
AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC  
AAGCCTGTTTTTTTACTCAGGAACGTGTACACGACCAGTGCTACTATGGATTGTGGACATT  
CCTCTGTGGAGACCGTGGGAGAAGCTAAACAATTTTTTAAAGCCCATATGGATTTAGTCAT  
CTGAATATGTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT  
TTTCTCTAGTATTATGTTTGATTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

**FIGURE 139**

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQSVSVNNEHNVANVDNNNGWDSWNS  
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQGKGPGGPPFKGLMYSVN  
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

**Signal Peptide:**

amino acids 1-20

**N-myristoylation Sites:**

amino acids 67-72, 118-123, 163-168

**Flavodoxin protein homology:**

amino acids 156-174

139/330-226860

**FIGURE 140**

CATTCTGAACTAATCGTGTGACAGAACTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA  
 TTAACTTTTTAGGAGTAATTTCTAGTTTGGAATGTAATATGAAATAATTTAAAAGGGCTTCG  
 CTCATATATAGGAAATCGCATATGGTCTAGTATTAATTTCTTATTGCTTACTGATTTTTT  
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA  
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG  
 CAAGCTTATAGTTGAAATATTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT  
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT  
 CAGATTCCGTTGCCAACTCGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAT  
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC  
 TGGAAAAAGAAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA  
 TTGAATCCGGATGGAATCCAGCCCTTCAACCTGGGTGGATTTCTCCAGCCTCCAAGCC  
 ATCATACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG  
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCAAAAAGCCCTTACAATGGTGTAAGAAAA  
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG  
 TTCTAGATCACAATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA  
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGCCCTCGAAGACATCATAATCAT  
 GGTTCCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG  
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG  
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT  
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG  
 CTGAATTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT  
 ATGGACTCAATCAAAAACATTAAACGCAAACTGATTAGGATTTGATTTCTTGAAACCTCTA  
 GGTCTCTAGAACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT  
 AAAATGCCTTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT  
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATCTGTAAAAATGTATCTTATTTTT  
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTGTTTAAATGATGGTGAAT  
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAGATTTTTACAAGGAAATAAAATACAAAT  
 CTTGTTTTTTCTAAAAAAGG

MNDSLRTNVFVRFPETIACACIYLAARALQIPLTRPHWFLFGTTEEEIQEICIETLRLY  
TRKKNPYELLEKEVEKRVQLQEAQLKAKGLNPDGTPALSTLGGFSPASKPSPSPREVKAEK  
SPIISNVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSASRASRSTRSRTRSRSRSHTPRRHY  
NRRSRDGYSSRRSRSRSHSESPPRRHHNGSPHLKAKHTRDDLKSSNRHGHHKRRKSRSRQ  
SKSRDHSDAAKKHHRERGHRRDRRERSRSPFRSHKSKHHGSGRSGHGRHR

**FIGURE 142**

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGCCTTAAAGATTATTGGAAGGGGTTTATCA  
TTTTTTGAANNTATTCGGGT CANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT  
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT  
CATATATAGGAAAATCGCATATGGTCCTAGTATTAATTTNTTATTGCTTACTGATTTTTTTTG  
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA  
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA  
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT  
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA  
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAATCC  
AGGAAATNTGCATAGAAACACTTAGGCCTTATACCAGAAAAAAGCCAAACTATGAATTACTG  
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTTAAAGCAAAGGGATT  
GAATCCGGATGGAACCTCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

**FIGURE 143**

GGACACGAGGCTCGTGCCAAAGCTTGGCACGAGGGTGACCCGCTTCTCGCACGCGTC**ATGGC**  
 GGTCCTCGGAGTACAGCTGGTGGTGACCCGTGCTACTGCCACCCTCATGCACAGGCTGGCGC  
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGATACAAGCACCCG  
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGAAAGAGCGGTG  
 GGCCAAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCCGTTCCAGCTGG  
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCAGTGG  
 TTTGTGGACTTTGCTGTGTACTCGGGCGCGTGTACCTCTTCACAGAGGCCTACTACTACAT  
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT  
 CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTTCAGCGCCGAGGAGGGGGTGAGCGC  
 TCTGTCTGCCTCACCTTTGCCTTCTTCTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGGC  
 GGAGGAGACCTCGAGCTGGGGCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC  
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAAGCTGGGTATCCGCGTG  
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCCTCACCTTCCCAGGCCCTGGCGCTGGC  
 CCAGACCCACCGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTG  
 ACACAGCTTCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCATTGCACGGGAC  
 TTCCTGCACAGCCGCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCCTCGA  
 CTCTGGGCGCCTCTGGTTGCTGGTGGTGGTGTGCTGCTGCTGCGGCTGGCGGTGACCCGGCCCC  
 ACCTGCAGGCCATACCTGTGCCCTGGCCAAGGCCGCGGTGGAGCAGCTGCGAAGGGAGGCTGGC  
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT  
 GAGCTTGCAGTACCTGACGCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC  
 TGGGAGGCTATTCTGGGGCCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC  
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG  
 GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCGTGGCGTCTGCGCTACCTCATCTGGT  
 GGACGGCTGCTGCCAGTGTCTCGCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA  
 GGCTCCT**TAG**CTGCTGCAGACCTCCTGGGGCCCTGAGGTCTGTTCTCTGGGGCAGCGGGACA  
 CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC  
 GCGGTTCCCTTACCCACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA  
 GAACTGTCTCTCCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG  
 TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAGGAGCATGCC  
 GATTTTTTAA

**FIGURE 144**

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEEELRALAGKPRPRGRKE  
RWANGLSEEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY  
YMLGPAKETNIAVFWCLLTVTFSIKMFLT VTRLYFSAEEGGERSVCLTFAFLFLLAMLVQV  
VREETLELGLEPGLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFLT FPGLR  
LAQTHRDALTMSEDRPMLQFLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA  
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT  
VVS LQYLTPLILTLNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI  
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLGS



CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC  
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGTGCTGTGTAACGGCAGTT  
TGTTCGATACAAGCACCCGNTTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC  
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC  
GAGATGCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGAATGCCCTGGTCTCGCG  
TTCTTCTCGGAGTACCAGTGTTTGTGGACTTTGCTGTGTACTCGGGCGCGGTGTACCTCTT  
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT  
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTCTGACAGTGACACGGCTGTACTTCAGC  
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGTGGC  
CATGCTGGTGCAAGCG

**FIGURE 146**

GGTTCCTACATCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCCGTGATTATTAACGTGGCTT  
 AATCTGAAGGTTTCTCAGTCAAATCTTTGTGATCTACTGATTGGGGGGCATGGCAAGGTTTGCTTAAAGGAGC  
 TTGGCTGGCTTTGGGCCCTTTAGCTGTACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGG  
 CGCTTCTGTTGCTGGTCTTGCCCTTGGCTCAGTCTCTGTAACATACATTGACAAATGTGGGCAACCTGCACCTCTCTG  
 TATTGAGAACTCTGTAAGGCTGCTCCCACTACGGCCTGACCAAGATAGGAAGAGGCGCTCACAAGATGGCTG  
 TCCAGAGCGCTGTGCGAGCCTCAGAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA  
 TGACAGACGAGCCTGGCCTAGACACACCTTGCCTACGTCTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCA  
 GTGGACTCTGGCCGGAGCAACCGAATAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA  
 AAAAAATAATCGAGCTTTGAGTGTCTTCGAGGAGCAAGAGCGGGAGTGCACTTGCCAAACCATGCCGACGAGG  
 GCAGGGAAAATTTGAAAACACCACCTGCCCTGAAGTCTTTCCAAGTTGTACCACTGATTCCAGATGGTGAA  
 ATTACAGCATCAAGATCAATCGAGTAGATCCAGTGAAAGCCTCTCTATTAGCTCGTGGAGGTAGCGAAAC  
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGCTACTGCCAG  
 GAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCTCGCGG  
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGAGCAGGAACAATGGACAGGCC  
 GGTGCTTACAGACCCCGAGATGACAGCTTTCATGTGATTCACAACAAAGTAGCCCCAGGAGCAGCTTGGAA  
 TAAAACTGGTGCAGAGTGGATGAGCCTGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA  
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAG  
 TGGCGCTCATCTGATTGAGGCAGTGAAGACGTGTTCACTCGTGTGCCAGGTTGGCAGGGGAGCC  
 CTGACATCTTTGAGGAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGGAGGACACAT  
 CCCAAGCCCTCCATCTCAATTTACTTGTCTATGAGAAGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT  
 CGGCATGACCGTCCGAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTGAGCCCG  
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTGTTGAATGTGGATGGGGTGAAGTGACA  
 GAGGTGAGCCGAGTGGGAGTGGCATATTGAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGT  
 CAAAGAGTATGAGCCCGAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCAACATGGCCCCACCA  
 GTGACTGGTCCCCATCTGGGTGATGTGGCTGGAATTACACCGTGCTTGTATAACTGTAAAGATATTGATTA  
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAACAAACCTTT  
 TTTCTCAATCAATCTGTTGAAGGAACACCAGCATCAATGATGGAAGAAATAGATGTGGTGATATCTCTCTTG  
 CTGTCATGCTAGAAGTACATCAGGAATGATACATGCTTGGTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA  
 ATTACTCTAATATTGTTCTTGGCCTGGCAGCTTTTTTGAAGATCAATGATGGGTGAGAGGAAACAGAAAAA  
 TCACAATAGGCTAGAAGTTGAAACACTATATTATCTTGTGAGTTTTATATTTAAAGAAAGATACATTTGT  
 AAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATGATTCCAAAAAATTA  
 AAACCTACTAGTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTACAACATTTGTTATATTTTCTATTTCAAT  
 AAAAGCCCTGAAACCACTAAATTTGATTTGATACCCCACTGAATCAAGCTGATTTAAATTTAAATTT  
 GGTATATGCTGAAGTCTGCCAAGGTGACATATGGCCATTTTTATTTACAGCTAAAATTTTTTAAATGCA  
 TTGCTGAGAAAGCTTGTCTTATCAACCAAGAAATAAATTTTTTCAAGTAA

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MKALLLVLPWLSPAYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT  
 APSPEVSAATISLMTDEPLDNPAYVSSAEDGQPAISVDSGRSNRTRARPFERSTIRSR  
 FKKINRALSVLRRTKSGSAVANHADQGRESENTTAEVFPRLYHLIPDGEITSIKINRVDP  
 SESLSIRLVGGSETPLVHIIQHIYRDGVIARDGRLLPGDIIKLVNGMDISNVPHNYAVRLL  
 RQPCQVLWLTVMREQFKFSRNRNGQAPDAYRPRDSSFHVILNKSSPEEQLGIKLVKRVDEPGV  
 FIFNVLDGGVAYRHGQLEENDRVLAINGHDRLRYGSPESAHHLIQASERRVHLVVSQRVQRS  
 PDI FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVNNIQKDPGESLGMTVAGGASHRE  
 WDLPIYVISVEPGGVISRDRIGTKDILLNVVGVELTEVSRSEAVALLKRTSSSIVLKALEV  
 KEYEPQEDCSSPAALDSNHNMAPSDWSPSWMWLELPRCLYNCKDILVRNLTAGSLGFCIV  
 GGYEYNGNKKPFIFKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGR  
 I  
 TLTIVSWPGTFL

**FIGURE 148**

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCATATAAAGGATAGAAGCT  
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCCTCTCCAGGCAAATGGTGCTGACCATCT  
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC  
AATGTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC  
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC  
TCTCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT  
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG  
GGTCAAGTACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC  
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT  
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG  
TGCAGACATTGATTTTAGGATGATTAGCCCTCTTGTTTTATCTTTCAAAGAAATACATCC  
TTGGTTTACACTCAAAGTCAAATTAAATTCTTTCCCAATGCCCAACTAATTTTGAGATTC  
AGTCAGAAAATATAAATGCTGTATTATA

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MKILVAFVLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT  
 IFDYKHGYIASRVLRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE  
 SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAGAGLLGILGISICADIHV

**FIGURE 150**

GGCACGAGCCAGGAAC TAGGAGGTTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC  
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG  
 GGAGGAAGAAATTACCCCTGGTCTCCATTGCCTACAAAGTCTTGGAAAGTTTCCCCAAAG  
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACGCCCATCACCTATTCCCTC  
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGTTGAAGACCCACGAGCCGGCCTCCTT  
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCTCCT  
 CCACCTCAGGTGCCATGTGGACAGTCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG  
 CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA  
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATACCAACAGCCTGATCGGGAAGGATG  
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG  
 AGCCAGACATCGGACTGTTCTGGTGCCAGGCTGCAAAACAACGCCAATGTCCAGCACAGCGC  
 CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAAGATGGAGGACTGGCAGGGTCCCCTGGA  
 GCCCCATCCTTGCCCTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG  
 GGGTTCAGGATAGGAATGGGGAGGTCAGAGGACGCAAAGCAGCAGCCATGTAGAATGAACC  
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCCTGTTTCGTATTGGA  
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

**FIGURE 151**

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL  
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK  
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCRQPANFSFLP  
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG  
GFRIGNGEVRGRKAAAM

**Signal Peptide:**

amino acids 1-18

**N-glycosylation Sites:**

amino acids 86-89, 132-135, 181-184

**FIGURE 152**

GGTCCTTA**AATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG  
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCCTCACTCTCTTTGCTATGACATCACCGT  
 CATCCCTAAGTTCAAGACTTGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA  
 CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTGACGTCCCCTGGGGAAGAAA  
 CTAAATGTCAACCGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT  
 TACAGAGCAACTGCGTGACATTGAGCTGGAGAATTACACACCCAAAGGAACCCCTCACCTGC  
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT  
 TTCGATGGGCAGATCTTCTCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC  
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT  
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC  
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCTTCAGGCACAACCCAACCTCAGGGCCAC  
 AGCCACCACCCCTCATCCTTTGCTGCTCCTCATCATCTCCCTGCTTCATCCTCCCTGGCA  
 TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG  
 GTCTTGATCAAATCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGATGTCCAGT  
 GGCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACGTGCCTTGATTCCTT  
 TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC  
 TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC  
 TCTTTTGTGTTGGAAAAATCAAGTACTTCTTTGAATGATGATCTCTTCTTGCAAATGATATT  
 GTCAGTAAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG  
 AATTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT  
 TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA



MAAAATKILLCLPLLLLSGWSRAGRADPHSLCYDITVIPKFRGPRWCVAQGGVDEKFTL  
HYDCGNKTVTPVSPLGKKNVTTAWKAQNPVLEVVLDLTEQLRDIQLENYTPKEPLTLQAR  
MSCEQKAEGHSSGSWQSFDFGQIFLLFDSEKRMWTVVHPGARKMKEKWENDKVVAMSFHYFS  
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTILCLLIILPCFILPGI

Signal peptide:

amino acids 1-25

## amino acids 224-246

## amino acids 68-72, 82-86

## amino acids 200-206, 210-216

## amino acids 77-81

GGGAAAGCCATTTCGAAAACCCATCTATACAACTATATATTTTCATTCTGCTGCTAGCTG  
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAGTTATATACCGTGGGAATGAGAG  
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACC AATTCTG  
GTGTGGCTTTCTTTGAGAGGATTCCACCTTCAAATCATGAACCTCGGCTGTTGATCAAAA  
GAGAAATTTGGATTCTACTCTAAAAGTCATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC  
TCAACCTGGCCTCCCATAAACAGGACAGATTATTAGGTGATGGCAAAATGGATTCTACAT  
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAAC TCAAATGGGAGGCCAAC  
CCACAGAACAGCATTTCTGGGCCAGGCTGTAACTCAGAATTGTCGTCGTACATGCTCAACAGC  
ATTGCTTTTTTCCCAAATTAACACATTTGTGGAGAAGTGATGATACCTCTGCCCTTACCTTT  
CCTCTCTCATTCACGATTCAAAGTATATTTTCAATGAATTAACCTTCGCAAGGAGACC  
TTAGATAGGCTTATCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCCCTGTAT  
CATCCTTTTCAATAAACTGTATTCTATTTGAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 155**

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHLEWLLIKREFGFYSKSQYRTWQKKLA  
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

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**FIGURE 156**

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**  
 CTCTTGTGGCAGGTAACTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA  
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCTCAGCCGGGCCCC  
 AGAACTGCCCTCCGTTTCTCTGTGCAGTAACCAAGTTCAGCAAGGTGGTGTGCACGCGCGG  
 GGCTCTCTCCGAGGTCCGCGAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA  
 CAACATCCAGATGATCCAGGCGACACCTTCCGCCACCTCCACACCTGGAGGTCTGTGAGT  
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCTTCAACGGCCTGGCCAGCCTCAAC  
 ACCCTGGAGCTGTCGACAACTGGCTGACAGTCATCCTAGCGGGGCTTTGAATACCTGTC  
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCCTCA  
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGAGCTCAAGAAGCTGGAGTATATCTCT  
 GAGGGAGCTTTTGGGGGCTGTCAACCTCAAGTATCTGAACCTTGGGCATGTGCAACATTAA  
 AGACATGCCCAATCTCACCCCTTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT  
 TCCCTGAGATCAGGCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTATG  
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTACGGGGCTGGCTCACTTGTGGAACCT  
 CAACTTGGCCCAATAAACCCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC  
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTTCTGTGGCTAGCC  
 TGGTGGCTTCGAGAGTATATACCACCAATTCCACCTGCTGTGGCCGCTGTATGTCATGCCAT  
 GCACATGCGAGGCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGTCTGTCCCTCT  
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCCGATGGCAGAACTTAAGTGT  
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGCTGCCAATGGGACAGTGTCTCAGCCACGC  
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACAGTGTCTGC  
 TTTGAGCACTGGGGGTACACATGCATGGTGACCAATGTTGACGGCAACTCCAACGCCTCG  
 GCCTAACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTCAACCAAGT  
 AACAGTGAGGACACGAGATCTCGCCTGAGGACACACGCGGAAAGTACAAGCCTGTTCCCTA  
 CCACGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGTCTTACAGACTACC  
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT  
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGTAG  
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACACGAGCGGAGTACAGTC  
 ACAGCCGCGCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC  
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGTCTGCCACAATTC  
 ATGACCATATTAACACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGC  
 CTCGGGAACCTCTGTGACCCACAGTCACCACTATCTGAACTTATATAATTCAGACCCA  
 TACCAGGCAAGGTACAGGAAACTCAAAAT**TGA**CTCCCCCCTCCCAAAAACTTATAAAAT  
 GCAATAGAAATGCACCAAGACAGCAACTTTGTACAGAGTGGGGAGAGACTTTTCTTGTGA  
 TATGCTTATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAAGA  
 CAAAAGTCAAAACA

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**FIGURE 157**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT  
RRGLSEVPQGI PSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS  
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY  
ISEGAFEGFLNLYNLGMCNIKDMPNLTPLVGLEEELEMSGNHFP EIRPGSFHGLSSLKKLW  
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLP HDLFTPLRYLVELHLHNPWNCDCDILW  
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFOCSAPFIMDAPRDLNISEGRMAEL  
KCRTPPMSSVKWLLPNGTVLSHASRHRPRISVLNDGT LNF SHVLLSDTGVYTCMVTNVAGNSN  
ASAYLNVSTAE LN TSNYSFFT VTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ  
TTRVPKQVAVPATDTTDKMQTSLDEVMTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRS  
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYN TYKFAHGAHWTE  
NSLGNLHPTVTTISEPYIIQTHTKDKVQETQI

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[illegible]

**FIGURE 159**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENINIMCRECCEYDQIECVCPGKREVV  
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD  
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD  
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLHFHSDGSKNFDGFAIYEEITACSSSPCFHDG  
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV  
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH  
QLYSAAFSKQKLQSAPTKKPALPFGDLPNGYQHLHTQLQYECISFPFYRRLGSSRRTCLRTGK  
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAATYRRTSGVHDGSLHKGAWFLVCSGALVNE  
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD  
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSG  
VVSVDLSLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR  
WHLMGLVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK

**FIGURE 160**

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAAGCTCAACTTGA  
 AGCTTTCTTTCGCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC  
 TTCAACCTGACTTTCCACCTTTCTCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCT  
 GACAGTGGTTGGGTGGGCCACCAGTAACACTTCGTGGGTGCCATTCAAGAGATTCCCTAAAG  
 CAAAGGAGTTTCATGGCTAATTTCCATAAGACCTCATTTTGGGGAAGGAAAAAAGCTGACT  
 AATGAAGCATCCACGAAGAAGGTAGAAGTTGACAAGTGTCTTCTGTGTCTCTTACCTCAG  
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC  
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC  
 CTCGTTCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT  
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGGTAAGAAAGT  
 TTAATCGAGCCAAACTCTTGAATGTGGGTATCTAGAACCCCTCAAGGAAGAAAAATGGGAC  
 TGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA  
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG  
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT  
 AACAACTACTGGGGATGGGGAGGCCAAGACGATGACCTCAGACTCAGGTTTGAGCTCCAAAG  
 AATGAAAATTTCCCGCCCCCTGCCTGAAGTGGGTAATATACAATGGTCTTCCACACTAGAG  
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCCAGAGTCTGG  
 AGACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA  
 TATCAACATCACAGTGGATTTCTGGTTTGGTGCATGACCCCTGGATCTTTTGGTGATGTTTGG  
 AAGAACTGATTCTTTGTTTGAATAATTTTGGCTAGAGACTTCAAATAGTAGCACACATTA  
 AGAAGCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTGTATTTTCTTAGCAGAGCT  
 CCTGGTGATGTAGAGTATAAACAGTGTGAACAGACAGCTTCTTAGTCATTTTGATCATG  
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGAT  
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT  
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGCTGAGAGAACCAGAGTTGTTCT  
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTTCATTTATCCTGTACAATCATCT  
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCCAGCAATCA  
 GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG  
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT  
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGA  
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACTAATAATAAATA  
 TGCTATCAAATACCTCTGTAGTAAATGTGAAAAGCAAAA



**FIGURE 161**

MGFNLT FHLSYKFRLLLLLTLC LTVVGWATSNYFVGAIQEIPKAKEFMANFHKT LILGKGKT  
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVAENPKVSRGRYRPQECKALQRV  
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIVIHQAEGKKFNRAKLINVGYLEALKEEN  
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGGRNSTGYRLRYSGYFGGVTALSREQFFKVNG  
FSNNYWGWWGGEDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR  
VWRDGLSSCSYKLVSV EHNPLYINITVDFWFGA

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites:**

amino acids 4-7, 220-223 and 335-338

**Xylose isomerase proteins:**

amino acids 191-201

CGTGGGCGGGGTCGCGAGCGGGCTGTGGCGCGCCGAGGAGCAGCCGCCGAGTCTCT  
GAGCTCCAGTGCATTCCTCCCGCTCCGCCACCGTCTTCCCGCTCCGGGCGCCGCAATG  
GCCAGGACGTTGGTGCGCCCTCGCGCCATCTCTTGGCTGGCTGCCCTCTCCGCTGGCG  
CCCCGAGGGGTGGCCGAGGCCTGTATGAATCAATCTACACCGATAGCCCTTGCCACCA  
CGGAGGCGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGCCCTC  
CCCGCTGAGCCCACTTACCAGCTTCCACTGGATCACACCCCGCTGGTGCTTACTGSCAA  
GATGGAGAAGGGTCTCAGCTCCACATCCGTTGGTGGCCACAGTCCGCGGGGAACTCCCG  
TCTCTGTCTGGTCTAGCTGCGCTGACTGCTGGATGTGGCCAGCTGTGGCCAGGGGCTTTGT  
GTCTTCCCCATCAGAGATTCTCTGTGGGGGACCTTGTGTGTCACCCAGAACACTTCCCTAC  
CTGCGCCAGCTCTATCTACTAAGACCGTCTGAAAGTCTCCTTCTCTCCACGACCCGA  
GCAACTCTCAAGACGCGCTTGTTTCTCTACAGCTGGGACTTGGGAGCGGACCCAGATG  
GTGACTGAAGACCTCCGTGGTCTATTATAACTATTTCATCATCGGGACCTTCAAGTGAAGT  
CAAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGATGCCACGAGGCTGTGGAAGCAAGA  
CCGGGACCTTCTCCGCTCGTGAAGCTGAGGAAGACCTTCGAGGCATCCAAGTGTGGG  
CCCCCTCAATTCAGACTTCCAAAGATACCGTGACCTTGAACCTTCTGGGAGGCCCTCC  
TCTGACTGTTGCTGGCGCTCTCAAGCTGAGTGCTCCGCTGGAGAGGGGATGCCAC  
CTGTGTCCGTGGCCAGCACGCTATAACCTGACCCACACCTTCAGGAGCCTTGGGAGCTAC  
TGCTTACAGATCCGGGCGGAGATATCATCAGCAAGACAGTACCACAGATCCAGGT  
GTGGCCCTCCAGAACTCAGCGCGCTGTCTTTGCTTTCCCATGTGCTACACTTACTCTGTA  
TGTGTGGCTTCATCATGTATGACATGACCTCGGGAATGCCATCAGCAAAAGACATGTGGGAG  
AACC CGGAGGCCACCTCTGGGTGAGGTGCTGCTGCCAGATGTGCTGTGGGCTTTCTTGG  
GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACACGGGCTGCTCCGCGCCCTCT  
ATAAGTCTGTCAAAATTCACACCTCTGAGCACTCCCCCTCCCCACCCCATCTCAGTGTAA  
CTGACTGCTGATCTGGAGTTTCCAGAGGGTGGTGTGACCACTGACCAAGAGGGGTTCAAT  
TGCGTGGGGCTGTGGCTCGGTGATCATTCATTCATCTGTACAGTTCAGCACTGCCACAAAGC  
CTTCCCTCTCTGTACCCCTGACCCAGCCATTCACCATCTGTACATCTGTACAGCACTGACA  
TAAGCCCCACTCGGTTACACCCCTTGTACCCCTTACCTTTGAAGAGGCTTCTGTGAGGACT  
TTGATGCTTGGGGTGTCCGTTGTGACTCTAGTGTGGCGCTGGCTGCCATGCCCATCTCTCT  
CTATATGGCAGATCTGCTGTTCATTTGGGGGTTCTCAGTTTCTCCCCAGACAGCCCTAC  
CTGTGCCAGAGAGCTAGAAGAAGGTCAAAAGGTTAAAAAGCTATAAGCTATAAGGTTGTAC  
ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACACACACACACAC  
CACACACACACAGAAATATAACACATCGCTGACATGGGCATTTCAGATGATCAGCTCTGTA  
TCTGGTTTAAGTCGGTGTGCTGGGATGACCCCTGACATAGAGTGAAGAAATTTGACCTCCA  
AGCAGCCCTGACAGGTTCTGGGGCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCAAGTCTTGC  
GCCCTTTATAAGGCCATCTAGTCCCTGTCTGCTGCGAGGGGCTGTGATGGGGGGCAGGACT  
AATACTGAGTGATTCGAGAGCTGTTATAATATCACCTATTTTATCGAAACCCATCTGTG  
AAACTTTTCACTGAGGAAGAAGCCCTGCAGCGGTAGAAGGTTTGAATCAAGCCGGGCGCGG  
TGCTCTCAGCCTGTAATCCGACACTTTGGGAGCGGCGGAGCGGTTGAATCAGAGATCAGGA  
GATCGAGACACCCTGGCTGACACCGTTGAACCCGCTCTACTATAAAAGATCAAAAAGTT  
AGCCGGGCGTGGTGGTGGGTGCTGTAGTCCAGCTACTCGGAGGCTGAGGCAGGAGATG  
GTGCGAAACCGGGAGGCGGAGTTCAGTGAAGCCACAGTGGCGCCACTGCACCTCAGCCTGA  
GTGACAGAGCGAGACTCTGTCTCCA

**FIGURE 163**

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA  
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHPGEFPVSVVWTAADCWMCQPVARGF  
VVLPITEFLVGD LVVTQNTSLPWPS SYLTKTVLKVSFLLHDP SNFLKTALFLYSWDFGDGTQ  
MVTEDSVVYNYNSIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL  
GPTLIQTFQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD  
YCF SIRAENIISKTHQYHKIQVWPSRIQPAVFAPPCATLITVMLAFIMYMTLRNATQQKDMV  
ENPEPPSGVRCCCMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 339-362

**N-glycosylation sites.**

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

**FIGURE 164**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACCTGAGCTCCCAGATCT  
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA  
CAACAGACGGGACAACCTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG  
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCT  
GCGGCTGCTGTATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG  
CCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCAGAACATAGGTCTTGGAATAAAA  
TGGCTGGTTCTTTGTTTTCCAAA  
AAA

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**FIGURE 165**

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH  
FPICIFCCGCCCHRSKCGMCCKT

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**FIGURE 166**

CTGTGAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCCTGGC  
 CTGGATCTTCCACC**ATG**TTCTCTGTGTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC  
 ATCTCCCTGACTGTCTCTTACCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG  
 AGTCTCCTTTGGTATCCGCCAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA  
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACACCAGCTTTACAGCCCTACACCAAC  
 GGAATCATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAGAGATTTCGTCGAAGTGG  
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGGC  
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAAGTGG  
 GAGTCTTGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC  
 GGTCTGTGGGGTTAGGAGTGTGATTTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC  
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT  
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCAATGTGTTACCGGATCTCGCTGCG  
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAACAGACCAAGAAATGGTGGCATCT  
 GTGTGGCCAAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC  
 ATGGTGGGTCAAGTGACCGGGGACTCATGGGTGTGATTACAGAGACCATGGTGAAGGCTG  
 CCCACAGCTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA  
 CTGAACATGTGCARGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC  
 AATAATACATCGGTGATGTGTTCAAAAAGGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC  
 TGTGTCTATCAAGTATGACCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA  
 TGGTGACGTACTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG  
 CCTCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTCTG  
 CATTGCCAGGCGAGGAGGACTTGTGGACCTGCTGTGGGATGGGGCCCTGAAGAGGGAGAAGG  
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCAC  
 AAGGACAGGAGCCGCTCCT**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCCTGCGGGGTGCCAA  
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCACTGCTGTGCTCTTCCAGACTCCAGGG  
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCCGCCAGCCGACGCGGATCCCTGT  
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA  
 CGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA  
 CCTTTGCACGCTGTGCGGGCTGAGTGGTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT  
 GGCCTGACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGCGGCCACCCG  
 CTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCTTCAACATCGCCCCAGC  
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCTATCTGCAGGGGCTTTGAGCAAAATG  
 AAGGGTTAGATTTTATCTGCTGCTGATGGGGTTACTAAAGGGGGGAAGGCGCAGGTG  
 GGCCGCTGACTGGGCCATGGGGAGAAGCTGTGTTCTGTAAGGCTTAACCTTGAATCCCC  
 ATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCATCTGTAATATGAGTCGGGGG  
 GAATGGTGGTACCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGA  
 AGGACATACAGTTCACTGTTTCAAGTACAGGCCCAAAAACGGGGCAGCGAGGCTGAG  
 CTCAGAGCTGCTGCACTGGGCTTTGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGA  
 TGA

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**FIGURE 167**

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME  
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKGME  
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLR LTVLWGLGVLIRYCFLLPLRIALFTG  
ISLLVVGTTVVGYPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRP RNGGICVANH  
TSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ  
DKSKLPILIFPEGTCINNTSVMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL  
LRMTSWAIVCSVWYLP PMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF  
KEEQQKLYSKMIVGNHKDRSRS

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**FIGURE 168**

CCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTACCCGGACCCCTGGCCCTCA  
CGTCTCCTCCAGGG**ATG**CGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC  
ACCTGGCAGGCCAGGCTGTTCCACCATCCTGCCCTGGGCCTGGCTCCAGACACCTTTGA  
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG  
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC  
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT  
CTACACCAACTCATCGAACACCTTGTA TACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG  
GCTCCCGGGAGCTCTACATGAGGCACTTCCCTTCAAGGCCCTGCATTCTACCTGATCCGG  
GCCCTGCAGCTGCTGCGAGGCAGTGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG  
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGACTCTGTCCGCTTGGGCCAGT  
TTGCCTCCAGCTCCTTGATAAGGCAGTGGCCACAGATTGGGGAGAAGAGCGGGGCTGT  
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCTCCTCTCTGCCCCCTG  
GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCAGCTCTCAGGGGTGGGGCC**TGA**AAGTCCA  
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG  
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCAACCAGG  
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTTGCTATGTGATGGGGACTTCCT  
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA  
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA



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**FIGURE 169**

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEKAAPLLKEEMAHH  
ALLRESWEAAQETWEDKRRGLTLP PGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL  
YMRHFPFKALHFYLIRALQLLRSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS  
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTL LLLAPGEFQLSGVGP

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**FIGURE 170**

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA  
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG  
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC  
TATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCA  
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG  
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT  
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG  
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG  
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC  
CCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT  
GCGTTGCCAGGAACCTGTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT  
GAAGGTGCTGCTGATGACCCGATTCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCCCT  
CCTGCTCAGTCTCTTTGTAAGTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG  
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCCAT  
TCTGGAGAGAAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA  
TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAATCCCCACTCAC  
TGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG  
CACTCCCCTAAGTCTCTGCTCA

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**FIGURE 171**

MAGSPTCLTLIYLWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT  
IQPEGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYVLHV  
YEHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDEVYTWKALGQAANESHNGSILPISWRW  
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLW  
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPANTVYSTVEIP  
KKMENPHSLLTMPDTPRLFAYENVI

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**FIGURE 172**

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC  
 TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC  
 CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATAAC  
 AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA  
 GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT  
 GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG  
 AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG  
 ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGCCCT  
 GGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG  
 AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGACAGAAACTTCTCAAGCCCC  
 ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCT  
 GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC  
 TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA  
 ACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA  
 TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA  
 AGATGGAAAATCCCCACTCACTGCTCAGGATGCCAGACACCAAGGCTATTTGCCTATGAG  
 AATGTTATCTAGACAGCAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 173**

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT  
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA  
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA  
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA  
TTCCTTAGTTCCTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG  
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT  
ATACCTAAGACAGACTATGATAACTTTCCTTATGGCTCACCTCATTAACAAAAGGATGGGGA  
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA  
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT  
GCCAATCGTCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC  
ACTTCTCACCAGGACTCCACCATCATCCCTTCCATCCATACAGCATCCCCAGTATAAATTC  
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATCCAGTCTATCAACATGTTACC  
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCCTTGACAAT  
TTTTCATGAAATTATTCTCTTCTGTTCAATAAATGATTACCCTTGCACTTAA

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**FIGURE 174**

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIIILASDKREKIEEHGNFRLFLEQ  
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI  
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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**FIGURE 175**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA  
TGGATTACGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG  
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC  
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG  
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTCCTTTCAGTGTGATCA  
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC  
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA  
CATTCATCCAGAATCCTTCAACTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG  
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCAC  
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTATAGGTCTATTGCT  
TGTGTGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC  
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAAATGGGAATAAAATGTAAGTA  
TCAGTAGTTTGAAAAAAAAA

**FIGURE 176**

MTCCGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA  
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNA  
NCEFSCLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL  
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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**FIGURE 177**

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT  
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCATGCTCTTGTCT  
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC  
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG  
CACCGATCAGATATCTTTTAAGAAAACGACTCTCATTGAAAAAGTCCTGGTGAAATAGTGAA  
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC  
CTGATCTTCACTAAAAATGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCTGC

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**FIGURE 178**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV  
KHCTDQISFKKRLSLKKSWWK

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**FIGURE 179**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG  
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG  
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCCCTC  
GAACCTGTGACATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG  
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAACCACTGCAG  
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG  
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC  
TCATCACTCCAGGCTCTGCCACTACTTGCTGAAGCAGGACTGGCCTCCAGGGATGGCCTGA  
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC  
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG  
CCCCACCACCCCTCA

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**FIGURE 181**

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCC  
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC  
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCCTTCTATAACAAGTCCGCGCGGCTCC  
 AGTGTTTTCCACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT  
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGT  
 ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA  
 CCAATGCCTCAGTGCCTATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG  
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCGCCACCGTCGGATGCTGAC  
 GCGCGCCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAACA  
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGCGAGCAGTCTGCTGACATGTTTGAG  
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG  
 TCAGGAGAGGCCCCAGTGAATATATTGCCACCATCTTGAGGCTCAGTGCCCTTGAGAGAAAA  
 GAAGCCAGCATATCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC  
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTCTATCCGGGAGCGGCGCTCG  
 CACCTTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG  
 ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGAGATGAGGAT  
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC  
 CTGGGTCTGTACAACCTTTCGAGGCACCCAGAATACCAGGAGCGTGCCGACAGGAGGTGC  
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC  
 TTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG  
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC  
 TCATCGATATTATAGGGGTCCATACAACCCAAGTGTGTGGCCGGATCCTGAGGTCTACGAC  
 CCCTTCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCTC  
 CGCAGGGCCCAGGAAGTGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCTCGG  
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA  
 TTGATCATGCGCGCGAGGGCGGGCTTGGCTGCGGGTGGAGCCCCGTAATGTAGGCTTGCA  
 GTGACTTTCTGACCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAGCGTGCTGTCAA

**FIGURE 182**

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFFQPPKRNWFWG  
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF  
IRFLKFWLGEGLILSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLLASEGS  
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY  
LSHDGRRFHRACRLVHDFDPAVIRERRRTLPTQGIDDFKDKAKSKTLDIFIDVLLSKDEDG  
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLAHPEYQERCQEVQELLKDRDPKEIEW  
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW  
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT  
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

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CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC  
TGTTTGCTTTTACAGGATTCTTAAATCCTCTCTTATCTCTTCTCTCCTTGACTCCAGGGA  
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGAGGAGCTAGAAA  
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG  
AAAGCAGACTCAAGTACCAACATTTTTAACCCAGAGGAAATTTGAGAAAGTTTCAGGATTT  
CTCTGGACAAGATCCTTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA  
AGAAACGTGAGACTCTGATTGCTTCTGGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT  
TAGTCAGCTCAGAAACCCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAAC  
AGTGTGGAGAAAAACTAGGCCAACTACACCTGTTCATTGTTACCTGGAAAAATAAATCCTCT  
ATGTTTGCACAAAAA

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**FIGURE 184**

MYKLASCCLLFTGFLNPLLSLPLLDSREISFQLSAPHEDARLTPEELERASLLQILPEMLGA  
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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**FIGURE 185**

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT  
GGGGTTGCTGTTTAAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA  
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCCCTCCC  
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT  
CCAGCTTCTTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA  
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA  
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT  
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG  
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGAATCGCCACAAGCCTTACTCACCTCTCTCT  
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA  
CAAGCTCAGGAGGCGAATAAATGTTCAAACCTGTA

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**FIGURE 186**

MPSPGTVCSELLLLGMLWLDLAMAGSSFLSFEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG  
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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**FIGURE 187**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC  
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAAT**ATGA**ACACGTGGTGCTGT  
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG  
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT  
 GAGTATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC  
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCAGCCTGGGGCCAGAGTCTTT  
 GTCCCCCGTGTGCGCATGTGTTCAAGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA  
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC  
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCT**TGA**AGTAACAAGTTTAAATGTTT  
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT  
 CCAAAAACACAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTACCCACTAACCA  
 AACAACCTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC  
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT  
 AACACAACCTCCCTGCTCCTGGCACCAGCCGTTTGGTCATGGTGGGCCAGCTGCAAAGCG  
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC  
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGCCCA  
 ACCCTGGTCAGGCAGAGGGAGTTGGGTGGGTCAGGCTCTGGGCTCACCTCCATCTCCAGA  
 GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA  
 GCCTCCTTGTTTCATAACCACAGGTTACCCTACAAACCCTGTCCCCACACAACCTGGGGAT  
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA  
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 188**

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLS PRSPQGW  
VVRAAHLTPLEYPNPEPPTPGARVFVPRVRMCSGASPRSEIMDKKGKSQEEIKSMRTQQ  
AQQEAELTPRPAGVVPGA

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GGAGTGCAGATGGCATGTCCTCTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGGCCAAAG  
ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCTATCTGCCATCCTCAGCATGCT  
ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG  
TGCCCAAGCCCTGTGCGAGAAAAGGCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG  
GATGGAGATACCAACACATCCACCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA  
CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG  
AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA  
GGACTACTGGAATTTGCCACGTTGCAAGGCCATGTCACCCCACTCTCCGATTTGGAGGGAA  
GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTTCCCTTGGGGCTTTGTGGCAAAAATGCTA  
TGTTTATCCTTGGAACGCAGATCACCTACATCGGACTTCAATTATCAGCTTCTCCTGCT  
ACTAACAGACTTGCTACTCAGTGGGAACCTGCCTGTGGGCTCAAACGAGCGCCTTTGCTG  
GTGTTTCCCTGTGCTGTGCTGCTGCTGCTGGGATGGTGGCCACATGATGTATTACAAGT  
TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTTATGGCTG  
GGCCTTCTACATGGCCTGGCTCTCCTTCACTGCTGCATGGCGTCGGCTGTCAACACCTTCA  
ACACGTACACCAGGATGGTGTGAGTTCAAGTGCAAGCATAGTAAAGCTTCAAGGAAAAAG  
CCGAACCTGCATTACACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC  
CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAG  
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTCAAAGAGGGGCCAGCCAGGAGCTG  
AAAGAAGCAGTTAGGTTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA  
GTAGGCTTGAGCCCTACCTTACAGCTCTGCTGATTATCAACATGTGCTTAAAGCCAACATCCG  
TCTCTTGAGCATGTTTTTACAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC  
CTAAGGAGATTCCTGGGTGCCATGCTCTCTTTCTCTACAGCTCCATCTTGTTTACCCAC  
CCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC  
TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

**F**

**F**

**F**

**FIGURE 191**

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCCAGATGTGGTTACCCCTTGGTCTCCTG  
TCTTTATGTCTTTCTCCTCTTCTATTCTGTCACTCTCCCTCACTTAAGTCTCAGGCCTGTCA  
GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG  
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT  
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG  
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCCCCTATTCTCTCTCCCAA  
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG  
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT  
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTACG  
GACATTGCCCCCTGTGTGCCACCAAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCT  
CTCCTGGTACCCAGCAAGACGTCTGTTCAGGGCAGTGTAGCATCTTTCAAGCTCCGTACT  
ATGGCGATGGCCATGATGTTACAATCCCCTTGCTGAATAATCAAGTGGGAAGGGGAAGCA  
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTGTGTTCTCCCTACCCTGAGGAAAAACCAA  
GGGAAGCAACAGGAACTCTGCAACTGGTTTTATCGGAAAGATCATCTGCCTGCAGATGC  
TGTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA  
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG  
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACTGCTGG  
AACCAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC  
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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**FIGURE 192**

MWLPLGLLSLCLSPILPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME  
HRNHLCFCDLYDRATSPPLKCSLL

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GTAGCGGCTCTTGGGCTCCCGGCTCGCGCTGCTGCGCGCGCGCTCGGGTCTGGAGCGAGGACGAGCTCA  
CGCGCATGTCAGGAGCATCAAGCTGTGTAATGATTGTCTTGTGCTTGGAGGACATFCGCACTGATGTTTTGATGGCT  
GGATGTGCCCTTCCAAATATAACAACAAATCTGGCGGCTTGTGTTCTATTTTTTACATCTCTTCACCTATTCC  
ATACCTGATATGCAAGAAGATTGATGGATGATACAGATGCTATGATGAACGCTGTGAAGCACTGCCAATCTTC  
TTACAACGGGATGTCGTGTGTCAGCTTTTGGACCTCCTATTGATGTCTCCGAGACACATCTGATTGAGTGGGGA  
GCTTGTGCACTTTGCTCTCACAGGAACAGATGCTTTGCACTATATCTAGGCTTTTCTGTCTTTGGAAG  
CAATGACGACTTTCAGTGGGACAGCATGGTCGAAGAAGAAATTCATGAACTATTTGTCATTTGAACTCTCTGCAAT  
TTGTGCCATTCACGCAACAGGAGATGGGCGAGTAAATGCTGAATGTATGACCAAGCTCTTGGGGATTTTT  
GGTGTCTCCTCTCTCACTTTTATGTGAAGCACTACTTTTACAGAGACTGTGTAAGGATTAAGAAGATTTCCT  
CTTTTGGAAAGTCTGACTGATTACACACTATCTATAGTATGCTTTTGTGGTGTCTCTGGAATTAATAAT  
TTATGTGTTTTCTGTGTATGTTGATTTTTTGGAAATGATATGCAATGTAAACACTTTTTTAATGATTAAT  
TTTGTCATTTGGTTAGGAATTCAGAATTCGCGCGCTCTATTACTGGTCAAGTACATCTTTCTCTAAAATTAAT  
TAGCCTTCATATTATAACAAAAATATAAAATAAGTTTTAGTCAGTCAGGATGACATCACTCCCAATGTATG  
CAGACATACAGACGGTGTGSCATGCTTATAGATAGCTATATACCTAGTGCAAATATAGCTGCATTTATACCTCAG  
GGCCAAAGTGTAAATGCCATACCGTCCGTTAAGGGTTGTGGTTTTCTGTTAGTACAGAGATGTTTTGTGGATT  
AAAAATTTTTATGAATGTGTCACAGAGAGTGCTTTCTCTCAATTTTGAAGAGATTTATGTAAACTTTA  
AGGTAAGGTTGTAAAAACATTTTTGAGTAAAGTTTTATGTATTTATTTATTTAGTAGGTGAGTGTCAATGT  
GGGAAGAAATGACATGAAATTCAGGTTTTGAACTCTGTTCCTATTATAGTGAAATTTGTGATCTCCATAT  
AOCCTTTCATGTTTTACCTCTTTAATAATGGACATCACTGAACCACTACTGAGTGGGGACAGTGTATGTGTTC  
ATCATATATGCGAAGAAAGCTCTCTCTGCTCTCTCTTGTACTTTATTTGGTATGTTATATATATACATAAAA  
TAACCTTTCAAATATAGTTTTAATACACTAGAAGTGTTCATCTACCTGAAAAATTAATGTATCTGCCGTACAT  
CAGAGTGGCCCCCTCCCTCGCAAGGCTCTGSCATGATTACAGTAAGTATGTAGTCTACAGATATATCATGCA  
TTAACAGTTTAAAGTTTAGACATGTAATAGTAGTTCTTATTCTCTAAGGTTATATCATATGTAATTAAGAAG  
TATTTTTAAGACAGATTTCTCTGTATACCTCTGAAGCTGTTTTGATTTGAGTTCATCATGATAGATCTGTGTTT  
CCCTATAAAGGCAATTTGTGTGTGAGTTAATCAAAAGTACGAAGTCCAGTATATAGACAGTCTGAAAGCAAT  
ACCTGACCAAAAAATTCAGATACCAAGCAGTATCAAAATATAGCTGTGCTTTTACATCTAATAATTTACAGGA  
CTTTTTTCAGGATGGGTTATAAAAAAATCAAGTGGTCTACAGATATTTGTGAAGATATTTTTGTGTATG  
TTTTATCAGTATACATACATAAAAAATTTATCGGCATCAGCCAAAATCAGTAATCATCAGACGCTGTCTGTGT  
TTTTAGAGTTTTATTCTCAAGAAAAATGGGAATAAATTTGGGATTTGTTCAGCTTTTTCTAAAGATGCTTAT  
AGCCACAGGTTTTATTGCTTAACCTTAAGCCATGACTTTTGAATATGAGATGACGGGAACGAGGACAGAAATCG  
CGGTGTGCTGGAGCCTCCCATCGAGGCTGAAGATGGCTGTGTGTTTATTAATGATTCAGATTTCAAGAGAA  
GGTGAGGATACACATGACTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTGTGCTTTGTGATCTAGGACTTT  
TTTTTTCAGGAAGTGCACTCTCTGTCGCTCTCCCTATTTCCTGTCGATGTGTCAGTGTGTCAGTGTGCTACTG  
TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTTTCTATACATTAATTCATTTGATGAGCAT  
GTGCTTTGACCTTGATATACGTTGACATAGTGCTGTCTGATTTTACGCTGATTTGATTTGATATGAT  
TTTCCATAGATATGACATGATACACATATCCCATCTCTCTATGGAAGAAAACCTTTGATGATGAACCAATAA  
AGATTTTAAATATCTATTTTAAAAAAAAAA

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**FIGURE 194**

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM  
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND  
DFSWQQW

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[illegible]

**FIGURE 196**

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNITEAPH  
NLSGLLGLSLRYNSLSELRAQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ  
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTLHMRANAQFVFPVRIQDCRS  
LKFLDIGYNQLKSLARNSFAGLFKLTLEHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIV  
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSITSIT  
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSG  
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA  
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH  
IEGALVIINEYGSCSCHQQPARECEV

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**FIGURE 197**

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC  
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA  
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCCGCTTGAGTTCCCGGCGGACAAGATGG  
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA  
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG  
CGCGGGCGAACCTGCCGTCTTCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT  
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC  
CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTCCGCGTGGGGCTCGGCCCTGGCGCTAG  
CCCCGTGCGTGTCCGCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG  
CTGTTTTCTGCGTCCCGCGGGCCGCTACGCTTCACGGGCCGGCGCGCT**TGA**CGCTG  
GGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGGAGCGCAGCCGTG  
GATCTGCGGGCCCTGCTCCAGCCCCT

**FIGURE 198**

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE  
GHAVSDMLLPDLGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA  
PGLFFVDAERVPCRHDDVFFPPSASFVGLGFGASPVVRVRSISALGRFTTRDEDLAVFLASR  
AGRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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**FIGURE 199**

ATCGCATCAATTGGGAGTACCATCTTCCTC**CATG**GGACCAGTGAAACAGCTGAAGCGAATGTT  
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTT  
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCA  
TTGACGTGGTACAGCCTTTCCTTCATACCATTTGCAAGGGATGCTGTGAAGAAGTGTTCG  
CGTGTGCTTGCA**TAA**ATTCATGGCCAGTTTATGAAGCTTTGGAAGGCATATGGACAGAAG  
CTGGTGGACAGTTTTGTAACATATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT  
TGCAGCAATGTGTTGCTTGTGATTTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACAT  
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA  
TCTTCCTCATGTACCTGTTTCCCTCTCTGGATGTTGTCCCACTGAATCCCATGAATACAAAC  
CTATTGAGCAACAGCAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 200**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP  
FARDAVKKCFVCLA

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**FIGURE 201**

TTGAGCGCAGGTGAGCTCTGCGCGTTCGCGGGCGGTCTCCAGTCAACCTCCCGCGGTACCCGCGGCGCGC  
 CCGAGGAGTCTCCTCCAGACCTCCCTCCCGTGTCTCAAACCTAATACGGACTGAACGGATCGCTGCGAGGGT  
 GGGAGAGAAATTAGGGGGAGAAAGGACAGAGAGAGCAACTCCATCCATAGCCAGATAGATTATCTTACACTG  
 AACCTGATCAAGTACTTTGAAATAGCACTTCGAAATTTATCTTGGTGTCTCTATACATCTGCTGACTGAGTCTTTC  
 AACCACTTTTCTCCAACTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACT  
 TATATAAAGTTCCACGCCCCATTTTCATATATATATGAATATGGTGTTCACGTGAAGCAAGTTACTATGTTT  
 TTTATTACAAAACCTCCCTTAACCATTATACTTTGGTAACTGSCCTCTTTGCAGAGAAATCATGGGATTGTTGC  
 AAATGATATGTTTATCCTTATTCGGAACAAATCTTCTCCTTGGATCAGATGAATATTATGATTCCAAAGTTT  
 GGGAGAGCGACACCAATATGATACAAACCCAGAGGCGAGGACATACCTAGTGGTGCAGCCATGTGGCCCGGA  
 ACAGATGTAAATATACATAAGCGCTTTCTCTACTTACATCGCTTACAAATGAGTCAGTTTCTATTGAGATAG  
 AGTTGCCAAAATTTGTTGAATGGTTTACGTCAAAAGAGCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCGTG  
 ATGACATGGGCCACCAATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCATTTAGATATTGACAAGAAAGTTA  
 GGTATCTCATACAAATGCTGAAAAGGCAAGTTGTGGAACACCTGTAACCTTAATCATCACAGTGATCATGG  
 AATGACGCGTGTCTGAGGAAAGGTTAATAGAACTTGACAGTACCTGGATAAAGACCACTATACCTGATTG  
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAACTCAAGCT  
 CATCTTAATCTTACTGTTTACAAAAAGAAAGACGTTCCAGAAAGGTGGCAATTACAAATACAACAGTCGAATTCA  
 ACCAATCATAGCAGTGGCTGATGAAGGTGGCACATTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACC  
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTGCTCTCAGAAAGAATTT  
 TCAAAAGAGCCATGAATCCACAGATTGTACCCACTACTATGCCACCTCTCTAATATCACTGCCATGCCACA  
 CAATGGATCATTTCTGGAATGTCCAGGATCTGCTCAATTGACCAATGCCAAGGTGGTCCCTTATACACAGAT  
 CTATACTCTCTCTGGTATGTTAAACAGCAGAAATGACCAAGAGGGGTATACCTTATTTCATAGGGGTC  
 TCTCTTGGCAGCATTATAGTGATGTTATTTTTGTATTTTCAATTAAGCATTAAATTCACAGTCAAATACCTGC  
 CTTACAAGATATGATGCTGAATAGCTCAACCATTTATACAAGCCTTAAGTTACTTTGAAGTGGATTGAT  
 TTGAAGTGGAGATTCATAATTTATGTCAGTGTAAAGGTTTCAAATTCGGGAAACAGTTCCAAACATCTGC  
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACACATACACACACAGGACCAA  
 ATACTTACACCTGCAAGGAATAAAGATGTGAGAGTATGTCTCCATTGTTCACTGTAGCATAGGGATAGATAAG  
 ATCTGCTTTTAAATTTCTCTCTGATGGTACTTAAATTTGAATGCACTTTATGGACAGTTATGCTTTATAAC  
 ATTGCACTTTAAATTTCTCTCTGATGGTACTTAAATTTGAATGCACTTTATGGACAGTTATGCTTTATAAC  
 TTGATTGAAATGCAACTTTTTCACCCATGTACAGAAATACCTGTTACGATGTTCAAACCTGAAGGAAAT  
 TCTAATTAATCCGAAATTAATGAACATAGAAATCTATCTCCATAAATTTGAGAGAAGAAGGTGATAAGTGTGTA  
 AAATTTAAATCTGATTAACCTTTGAACCTCTGAATTTTGGAGATGATTCCCAACAGCAGAATGCAACTGTGGGCAT  
 TCTCTGCTTATTTCTTTCCAGAGAACGTGGTTTTCATTTATTTTCCCTCAAAGAGAGTCAAATATCTGCAG  
 ATTCTTCTAAATATATTGTTTCTGTCATAAAATTTATTTGATTTCTGATGAGTCATATTACTGTTATTTCA  
 TTAATATGAGACACCATGAATATCTTTCTCTATATAGTTGACCAATGGCCGATACAGAACACAGGCA  
 CCATCTCAGCAATGTTTCTCTGTTTGTATTTTGTCTCTTTGAAATTAATCACTATTAAATACATTA  
 AAATCAAAATGGATAAAAAAAAAAAAAAAAAAAA

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MTSKFILVSFILAALSLSTTFSLQLDQQKVLVLSFDGFRWDYLYKVPTPHFHYIMKYGVHVK  
QVTNVFITKTPYNNHYLTVTGLFAENHGIVANDMFDPIRKNKSFSLDHMNIYDSKFWEATPIW  
ITNQRAGHTSGAAMWPGTDVKIKHRFPPTHYMPYNESVSFEDRVAKIVIEWFTSKEPINLGLLY  
WEDPDDMGHHLGPDSPLMGPVISIDIDKKLGYLIQMLKKAKLWNTLNLIIITSDHGMTQCSEER  
LIELDQYLDKDHYTELDQSPVAAIILPEKGFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN  
SRIQPIIAVADEGWIIHLNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNST  
LYPLLCHLLNITAMPFHNGSNFWQDLLNSAMRPVVPYTOQTILLPGSVKPAEYDQEGSYFYF  
IGVSLGSIIVIVFIFIKHLIHSOIIPALODMHAETIAPLLQA

## amino acids 1-22

## amino acids 429-452

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

## amino acids 69-85

## amino acids 212-241

GGATTTTTTGTGATCCGGAATTGCTCCACGGGCGGGACCTTTGTAACTGCGGGAGGCCGAC  
GACAGGCCACCTGCGGGGCGGGAGGCAGCGGGGTGAGGGAGGTGAAGAAACCAAGACGC  
AGAGAGGCCAAGCCCCTTGCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA  
CCAGATCCAGAGGCCAAGGGGACATGGCCACCTGGGACGAAAAGGCAGTACCCGCGAGGGCC  
AAGGTGGCTCCCCTGAGAGGATGAGCAAGTTCTTAAGGCATTACGGTCGTGGGAGACGA  
CTACCATGCTTGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG  
AGCAGCCACCACCACACCAGTCTCAGGCAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC  
CCTGCCCTTGGCCCCGACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTG  
CAGCTCCCACAGTTTTCAGGTCATCATCTGCTGTGGTGTTCTGGATGCCCTCTGTTGC  
TTGCTGAGTCACTCTTGACCTGAAGATCATCCAGCCGACAGAATAAATTAATGCTGCCATG  
GTATTCACCTACATGAGCATCACCATTCTGGTCTTTTTTATGATGGAGATCATCTTTAAATT  
ATTTGCTCTCCGCTGAGTTCTTTACCACAAGTTGAGATCCTGGATGCCCGTCGTGGTGG  
TGGTCTCATTATCCTGGACATTGTCTCTGTTCCAGGAGCACCAGTTTGGGCTCTGGGC  
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT  
TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA  
AGATTCAACACCTTGAGTTCACTGCTCTGAGAAGCCCTGGACTTGATGAGTTTGTGTATC  
AACCTGTAAGGAGAAGCTCTCTCCGATGGCATGGGAATGAAAGAATCCGACTTCTACTCT  
CACACAGCCACCGTGAAGTCTCTGGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG  
CAGGCTGGCATGTTCACTGGGCTGGTGTTACGACAGAGAACCTGACAGTCACTGGCCAGTTA  
TCACCTCAGATTACAATCACACAGAGCATCTGCCTGTTTTCAATCACAGAGAACAACC  
AAACTCTATAAGATATTCTGAAATATTGACAAATTTGACAAATAAAGGCATAAACGTGTA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 204**

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGGDYHAWNINYKKWENEEEEEEQPPPTPV  
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAEIIDL  
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFLSSFTTSLRSWMPVVVVVSFILDI  
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVQLAAKIQHLEFS  
CSEKPLD

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**FIGURE 205**

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGAGTGGAGCACCCAGCAGGCCGCCAACAT  
**G**CTCTGTCTGTGCCTGTACGTCGCCGTCATCGGGGAAGCCAGACAGGATTCACAGTACTTTG  
 AGTCGAAGGGGCTCCCTCGCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCCCTC  
 CAGGAATTCACCGCTACCGCAGTGAAGCAGAAAAATTGTACAAGCTGGAGATTAAGGACCT  
 TGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGA  
 GGCTGGTGTTTAAGATTTTGGACAAAAGAAATGATGGAGCAGTATGACCGCCAGGAGATCATG  
 CAGTCCCTGGGGACTTGGGAGTCAAGATATCTGAACAGCAGGCGAAGAAAAATTTCTCAAGAG  
 CATGGATAAAAAACGACGATGACCATCGACTGGAACGAGTGGAGAGACATACCACCTCCTCC  
 ACCCCCTGGAAACATCCCCGAGATCATCTCTACTGGAAGCATTCACGATCTTTGATGTG  
 GGTGAGAAATCAACGGTCCCCGATGAGTTCACAGTGGAGGAGAGGCGAGACGGGGATGTGGTG  
 GAGACACCTGTGTGGCAGGAGTGGGGCAGGGGCGGTATCCAGAACCTGCAACGGCCCCCTGG  
 ACAGGCTCAAGGTGCTCATGGAGGTCCATGCCTCCCCGAGCAACAACATGGGCATCGTTGGT  
 GGCTTCACATCAGATGATTTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGGCAATGGCATCAA  
 CGTCTCAAAATTCGCCCGGAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGGCC  
 TTGTTGGTAGTGACGAGGAGCTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCCCTGGCA  
 GGGGCCATCGCCAGAGCAGATCTACCCAAATGGAGTTCCTGAAGACCCGGATGGCGCTGGC  
 GAGACAGGGCCAGTACTCAGGAATGCTGGACTGCCCCAGGAGGATCTGGCCAGAGAGGGGG  
 TGGCGCGCTTCTACAAAGGCTATGTCCCCAACATGTGGGCATCATCCCCATTCGCCGCATC  
 GACTTTCGAGTCTACGAGAGCTCAAGAATGCCTGGCTGACGACATTCAGTGAAGCAACGCG  
 GAGCCCCGGGTGTTTGTGCTCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGGCTGG  
 CAGCTACCCGCTCCGCTAGTCAGGACCCGAGTCAGGCGCAAGCTCTATTGAGGCGCT  
 CCGGAGGTGACCATGAGCAGCCTCTTCAAACATATCTCGCGACCGAGGGGGCTCTGGGCT  
 GTACAGGGGCTGGCCCCAACTTTCATGAAGGTATCCCAAGTGTGAGCATCAGCTACGCTGG  
 TCTACGAGAAGCTGAAGATCACCTGGGCGTGCAGTTCGGGT**G**AGCGGGGGAGGGGCCGCCG  
 GCAGTGGACATCGCTGATCTGGGCCGAGCCTGGGGTGTGCAGCCATCTGATTGTGAATG  
 TGGCAACACTAAGCTCTCTGAGCCAAAGCTGTGAAAACCTAGACGACCCCGAGGGAGGGT  
 GGGGAGAGCTGGCAGGCGCAGGGCTTGTCTGTCTGACCCAGCAGACCTCTCTGTTGGTTC  
 AGCAAGACCAAGGCATTCCTTAGGCTCCAGGGTCAGCAGGCTCCGGGCTCAGATGTGTAA  
 GGCAGAGCAATTTCTGCACTGCTGCCAATAGTGAGCTTGGAGCTGGAGGCCGGCTTAGT  
 TCTTCCATTTCAACCTTGCAAGCAGCTGTTGGCCACGGCCCCCTGCCTCTGTGTTCCGCTG  
 ATCTCCCTGTGCCCTTCTGCTGCTGCTGTCTGCTGAGGTGAAGTGGGAGGAGGGCTACAG  
 CCCCACATCCCACCCCTCCTCCAATCCCATTAATCCATGATGAAGGTGAGGTACGTTGGCCT  
 CCCAGGCTGACTTCCCAACTTACAGCATTGACGCCAACTTGGCTGTGAAGGAAGAGGAAAG  
 GATCTGGCCTTGTGCTGATGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT  
 TGGGAGTCAGGGGGGCTCGGGCTGCCTGGCTGCACAGAAGCAAGTGTGGGGCTCA  
 TGGTGCTGTGAGCTGGCTGGACCCCTGTGAGGATGGGCCCCACCTCAGAACCAAACTCACTG  
 TCCCCACTGTGGCATGAGGCGAGTGGAGCACCATGTTTGAGGCGAAGGGCAGAGCGTTTGT  
 GTGTTCTGGGAGGGAAGGAAAAAGTGTGGAGGCTTAATTAATGACTGTTGGGAAAAAGGG  
 TTTTGTCCAGGAAGACAAAGCCGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAAGCAGG  
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTCTGACGCCCTGGGGGTTCTGTCCAAC  
 CCAGCAGGGCGCAGCGGACCAAGCCACATTCACCTTGTGCTGACTGCTTGGAACTTATTT  
 ATTTTGTATTTTATTTGAACAGAGTTATGTCTTAATACTATTTTATAGATTGTTTAAATTAATA  
 CTTTGTCAATTTCAAGTCTCATTTTTTATCATATTTATGTTTATGCTTGTATTTGACTTCCC  
 AAGCCCCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGGCCGCTGCAGTCACTC  
 CTGTCTCAGAAAAATTCCTTTTGGGACTGGAGGCGAAGAGCGGCCAGAGGCGACCCCTG  
 GCTCTGCTTCTTCTTGGCAGGTGGGGAAAGGGCTTGCCTCCAGCCTTAGGATTTACAGGTTTGA  
 CTGGGGGCTGGAGAGAGAGGAGGAACCTCAATAACCTTGAAGTGGAAATCCAGTTATTTT  
 CTGCGCTGCGAGGGTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAGTGGAGTGGCTCT  
 CAGTGTGAATTTGTGGTGGGGGGGCTGGAGGAGAGGTGGGGGGCTGGCTCGCTGCCCTCC  
 CAGCCTTCTGCTGCCCTGCTTAACAAATGCCGGCCAAGTGGCGACCTCAGGTTGCACCTTCC  
 ATTTCCACAGGATGACCTGATGAGGAATCTTAATAGGATGCAAGAGTCAATGACAAAAAT  
 GTTATATATGAACATATACTGGAGTCTGCAAAAGCAAAATTAAGAAGAATTTGGACGTAG  
 AAGTTGTCATTTAAAGCAGCTTCTAATAAAGTTGTTTCAAGCTGAAAAAAAGAAAAA  
 AA

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**FIGURE 206**

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD  
 LDGQLDFEEFVHYLQDHEKKLRLVFKILDKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK  
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMW  
 WRHLVAGGGGAGAVSRTCTAPLDRLKVLMLQVHASRSNNMGIVGGFTQMIREGGARS LWRNGI  
 NVLKIAPESAIFMAYEQIKRLVGSQETLRIHERLVAGSLAGATAQSSIYPMEVLKTRMAL  
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS  
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG  
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation site.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

**FIGURE 207**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT  
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATATTATTCTGGCTGGAG  
 CAATTGCACTCATCATTGGCTTTGGTATTTACAGGAGACACTCCATCAGAGTCACTACTGTC  
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAA  
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA  
 AAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTAGAGGCCGGACAGCAGTGTTT  
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTCGGGCTGAAAAACGTGCAACTCACAGATGC  
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA  
 AAAGTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG  
 CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA  
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAAGTCTGAGAATGTGACCA  
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACATACTCCTGTATGATTGAA  
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG  
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTTCTTTCTTTGCCATCAGCT  
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAATGTGCCTTGGCCACAAAAAG  
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG  
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA  
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAA  
 GACATATTAGAAGTTGGGAAAAATAATTCATGTGAAGTGAAGTGTGTTAAGAGTGATAAG  
 TAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT  
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG  
 TAATGTGTCTGTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTC  
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG  
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT  
 TGGCTTCTCTTCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA  
 ACAGAGCAGTCGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA  
 AA

**FIGURE 208**

MASLGQILFWSIISIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI  
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVI VGNASLRRLKNVQLTD  
AGTYKCYIIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD  
QGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESSEIKRR  
SHLQLLSKASLCVSSFFAISWALLPLSPYMLK

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**FIGURE 209**

GAATTTGTAGAAGACAGCGCGCTTGCC**ATG**CGCGCTCTCTGGGCGAGGTGTTGGCTCTGGT  
 GCTGGTGGCCGCTCTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCTCCGCCGGCCTGC  
 AGCGGGTTCATGAGCCGACCTGGGCCAGCAGTTGCTACAGGAGATGAAGACCCCTCTTCTTG  
 AATACTGAGTACCTGATGCCCTTTCTCCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC  
 CTGGGCATCGACAGATCTGACCTGGCTGTGCCATCTGTAACTCTCTGGCTATCATCTTCA  
 CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAAAGTAAGTTAGACTACTGC  
 GAGTGGGGGACGCAGCTCTGTGGATCTCGACATACCTGTGTTAGTTCTTCCCAGAACCCAT  
 CTCCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCCTGCCCTTTCTCTGCAGCTGTTTT  
 GCTTCTTGTGGCCATCAGAGTTCCCTTCCCCTGGACAGTCTGGAGAAAGACAGAGGCTGGG  
 GTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCTCCAGCCCTGTACCAGCTCCTACT  
 GGCATGGCTGAGCTCAGACCCCTCCTGATTTCTGCCTATTATCCAGGAGCAGTTGCTGGCAT  
 GGTGCTCACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGGC  
 AACAGTCTACCCTTTGAGTGGGCCGAACCCACTTCCAGCTCTGCTGCCTCCAGGAAGCCCCCT  
 GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTTCCCCCTCTCTGGCCTTAGCTT  
 CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAAGAGTGAAAG  
 AGTTTTGTAACTTCAAGTGCTGTTGAGCTGCGGGGATTTAGCACAGGAGACTCTACGCTCA  
 CCCTCAGCAACCTTTCTGCCCCAGCAGCTCTCTTCTGCTAACATCTCAGGCTCCCAGCCCA  
 GCCACCATTA CTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGA ACT  
 CCAGCTCAGTGGAAAGGGCCAGCTGCAGACTTGTAGCCAGAAATGCAAACGGGAGGCCTCTG  
 GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGGAAGAAGGTGCGTCGGA  
 GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTTGCTGCCCCACCCATGAGGTAGGCAG  
 AAATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC  
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAAACAGACAAAAAAAAAAAAA  
 AA

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**FIGURE 210**

MAASLGQVLALVLVAALWGGTQPPLKASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCSSLYYLTLASTDLTLAVPICNSLAIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFFILPFPLQLFCFLVAIRVPFPFVTVVRKTEAGVWD

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CTTCTGTAGGACAGTCAACAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG  
GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTCGAAAAGATTCCGCAATAAACT  
TTGCCAGTGGGAAGTACCTAGTGAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT  
TGAGGCCCTGTGGTCCCCATCCTGGGAGAAGTCAGCTCCAGCACCA**ATGA**AGGGCATCCTCG  
TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT  
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCCTCTGAATGTCCCTCACATGCCAACACCAG  
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACAGAATATGT  
TCTGCTCAGCGGAGAAGTCAGTGAGGAGACACACATTACAGCCTTCACTGTCCAGTGTC  
GCTGAAGAACACTTTTCATTTTGTAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG  
CGATGCCCTGGACCTTCCCCTGAAGAAGCTGTCCAGCAACGCAGAGTGCCCTGCTTGTATTG  
AATCTAATGGAACCTCCTGTCTGTGGGAAGCCCTGGAATGTCTATGAAGAAGAACAGTGTGTC  
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTT  
CAACGTCAGTAACGCCACCTGTCAGTTCTCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCA  
TCTTTCGAAAGTTTGAGTGTGCAATGTAAACAGCTTAACCCCCACGTCAGCACCAACCACT  
TCCACAACAGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGGCTTCTTCTCTG  
GGGACTGCTGCCCT**TCGAGG**TCTGGGGCTGCACCTTTCGCCAGCACCCCAATTTCTGCTTCTG  
AGGTCCTCAGAGCACCCCTCGGGTGTGACACCCCTCTTCCCTGCTCTGCCCGTTTAACATGC  
CCAGTAAGTGGGAGTCACAGGTCTCAGGCAATGCCAGACAGTGCCTTGTCTTCATTATTA  
AAGCACTGGTTCACTGCTGCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MKGILVAGITAVLVAAVESLSVCVQNSWEKSCVNSIASECPSHANTSCISSASSSLETVPVR  
LYQNMFCSAENCSEETHITAFTHVHSAEEHFHVSVQCQCKECSNTSDALDPPLKNVSSNAE  
CPACYESNGTSCRGPWKCYEEEQCVFLVLAELKNDIESKSLVLKGCNSVSNATCQFLSGENK  
TLGGVIFRKFECAVNSLTPTSAPTTSHNVGSKASLYLLALASLLLRGLLP

**FIGURE 213**

GGCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGAGCGAAGGTAGGAGGCA  
 GGGCTTGCCCTCACTGGCCACCCCTCCAACCCCAAGAGCCAGCCCCATGGTCCCCGCCGCCG  
 GCGCGCTGCTGTGGGTCTGTGCTGAATCTGGGTCCCCGGGCGGGGGGCCCAAGGCCTG  
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCGACG  
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA  
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACAGCGGCTGCCGAGCTCTTGGCCGCC  
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAAAGAGGAGGATGGGTCTTCAGAAGA  
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCGACTCCA  
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG  
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC  
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGCCGCTCACCTCACCCACAG  
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGCCACTGCCAC  
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCT  
 TCAGTTGGGGCGCTGAGCCAGCTCCGACGGAGCACAAAGCCTTGACCTATCAACAATGTC  
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCACTGT  
 GCCTCTCAGAGCACCAACAGTACCAGGACCACCTACCCCTTCCCCACCATCCACCTCAG  
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCCTGCCAGCCCTGGCTTTTTGGAACGGGTCA  
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA  
 GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT  
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAACTGGAAAA  
 CACAA

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 1000-1200

**FIGURE 214**

MVPAAGALLWVLLLNLGPRAGAQGLTQTPTEMQRVSLRFGGPMTRSyrSTARTGLPRKTRI  
ILEDENDAMADADRLAGPAAELLAATVSTGFSRSSAINEDGSSEEGVINAGKDSREL  
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP  
SPSPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC  
TYQQQPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA  
FWKRVRIGLEDIWNLSLVFTEMQPIDRNQR

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**FIGURE 215**

CCGGGTGCAGCCACGCGTCCGGGGAGAAAGCATGGCCGCGCTGGCGGCGGGTGGTCTGCTAGCTGGGGCA  
 GCGGCGCTGGCGAGCGGCTCCCAGGGCGACCGTGAGCCGCTGTACCGCGACTCGGTACTCGAGTGGCAAGAGCA  
 GAATGCTCTTGGGGCGCTCTGAATCACTTCCGCTCCCGCAGCCAACTACATGAGTCTAGCAGGCTGGACCT  
 GTCCGGGACGACTGTAAGTATGAGTGTATCTGGGTACCGCTGGGCTCTACCTCCAGGAGGTCAAAAGTGCCT  
 CAGTTCATGGGCAAGTGGCCCTTCCCGGTTCTCTTTCAAGAGCCGCGATCCGGCGTGGCTCGTGTCT  
 CAATGGCCCTGGCCAGCGCTGGTATGCTCTGCGCTACCGCACTTCTGTCACAGTCTTCCACACAGGACACTGAC  
 CCTGTGGGCGCTTCCGCTGGGTGCTCCCTCAATGCATGGTCTGTGCTCCAGTCTTACACTCAATCTACCTGTGCTGCGTCAGGAC  
 CTCACAGAGAAATGGACTACTTCTGTGCTCCACTGTCACTACACTCAATCTACCTGTGCTGCGTCAGGAC  
 CGTGGGCGTGCAGCACCAGCTGTGGTCAGTGCCCTTCCGGGCTCTCTGCTGCTCATGCTGACCGGTGCACGCTCT  
 CCTACCTGAGCGCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACTGGGCTATTGGGCTGGTCAACGCTG  
 GTGTGGTGGCTGGGCTGGTGCCTGTGGAACCCAGCGGCGGCTGCTCACGTGCGCAAGTGCGTGGTGGTGGTCTT  
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGTTGACTTCCCAACCGCTCTTCTGGGTCTGGATGCCATGCCA  
 TCTGGCACATCAGCACCATCCCTGTCCACGCTCTTTTTCTAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG  
 AAGGAATCAGAGGACAAGTTCAAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCC  
 GCCCTGCTGGGCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAAGTGGACATGA  
 AGGATGTGGGCCAGAACTCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGG  
 AAGGCTCCCGCATCTGGGACTCGAGAGTGGGCGCCCTCTACCTCTGGAGCTGAATGGGGTGGAACTGA  
 GTGTGTTCTTAGCTCTACCGGGAGGACAGTGCCTGTTCTCCCAACAGCCTCTCTCCCAATCCCAAGCTG  
 CCTGGCTGGTCTGAAGCCCTCTGTCTACCTGGGAGACAGGACACAGGCTTAGGGATACAGGGGGTCCC  
 CTCTGTATCCACCCCCACCCCTCTCCAGGACCACTAGGTGGTGTGGATGCTTTCTTTGGCCAGCCAA  
 GGTTCACGGCGATTCTCCCATGGATCTTGAGGACCAAGCTGCTGGGATGGGAAGGAGTTTCAACCTGACC  
 GTGTGCTTACGAGGTTCCAGGAGGCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCCAAGGCA  
 AGGATCTCTGTGCTGTCTGGTGTGAGAGCTGCCACCGTGTGTGCGGAGTGTGGCCAGGCTGAGTGCATAGG  
 TGACAGGGCGCTCAGCATGGGCTGGTGTGTGTGAGCTCAGGCTAGGTGCGAGTGTGGAGAGGGGTGTTGT  
 CGGGAGACGCTGTGGCTCAAAGTGTGTGTGTGACAGGGGGTGGGTGTGTAGCGTGGTTAGGGGAACGTGTG  
 TGCGCGTGTGTGGGCTGTGAGATGAGTGAATGCTGCTGCTGGTGGCCCTTTGCCCGCTCTGTCGAAC  
 GAGGGAATCTGTCACTCAATATCACTGTGGAGCGCAGCTCTGCCAAGACGCCACCTGGGCGGAGAGC  
 CAGGAGCTCTCAATGGCCAGGCTGCCTGTGTGATGTTCCCTGTCTGGTGGCCCTTTGCCCGCTCTGTCGAAC  
 CTCACAGGTCGCCACACAAGCTGCCCTCCAGAAGCAGCCCTCGGAGGCAGAGGAAGGAAATGGGGATGGC  
 TGGGCTCTCTCACTCTCTTTTTCTCTTGGCTTCGATGGCTGGCTTCCCTTCCAAACCTCCATTCCTCT  
 GCTGCCAGCCCTTTGCCATAGCTGATTTTGGGGAGGAGGAGGGCGATTTGAGGGAGAAGGGGAGAAAGCT  
 TATGGCTGGGCTGTGGTTTCTCCCTTCCAGAGGCTTACTGTTCCAGGGTGGCCCGCCAGGCGAGCGAGGGCC  
 ACATATGCTCTGGCCCTGGTAAAGGTGACCCCTGCCATTTACACAGCGCCCTGGCATGTTCTGCCCAACAG  
 ATAGAAATGGAGGGAGCTCCAGAACTTCCATCCCAAAGGAGCTCCGCTGTTGAGAGCAGACTGGATTTTG  
 CTCGCGCTTACCCCTTGTCCCTTTTGGGGAGGGAGCTATGCTAGGACTTCAACCTCAGGAGCTCGGGT  
 GCGTGCCTAGCTCTTTTGTACTGAAACTTTTAAAGTGGGAGGTGGCAAGGATGTGCTTATAAATCAA  
 TTCCAAGCTCAAAAAAAAAAAAAAAAAA

**FIGURE 216**

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW  
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSTRFLFFQEPASAVASFLNGLASLVMLCR  
 YRTFVPASSPMYHTCVAFWVSLNAWFSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR  
 TVGLQHFAVVSAFRALLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR  
 RLPHVVRKCVVVVLLQGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL  
 KESEDKFKLD

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

**N-glycosylation site.**

amino acids 40-44

**N-myristoylation site.**

amino acids 43-49

**CUB domain proteins profile.**

amino acids 285-302

**Amiloride-sensitive sodium channels proteins.**

amino acids 162-186



**FIGURE 217**

GGCCGCTTGGAAATGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGTCCGTGA  
 CT**ATG**GCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG  
 CTGATGGCGCCTGCTTCACCTTCTGCCCTCAGTCATCAGAACCTGAAGAGTTTGCCCTGAC  
 CAACCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAGAAAAGAAACCAAAGCCGAGGAGGAGC  
 TGGATGCCGAAGTCTTGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG  
 CAGGCTGTCCCTGCAGGATCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCCAAA  
 ACTCCAATATGAGGACAAGTTCCGAAATAATTTGAAAGGCCAAAAGGCTGGATATCAACACCA  
 ACACCTACACATCTCAGGATCTCAAGAGTGCCTGGCAAATTCAGGAGGGGGCAGAGATG  
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCGCCCCATTGA  
 GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTGCTATTGAGACTGACATGCAGATCATGG  
 TACGGCTGATCAACAAGTTCAATAGTTCAGCTCCAGTTTGGAAGAGAAGATTGCTGCGCTC  
 TTTGATCTTGAATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGG  
 TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCCCTCGTGAAGGAGTATGCTGCGT  
 TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGA  
 GCCCTGCAGAAGCTGCTGGTTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAGAAGGT  
 CCTGTTTGCACTGTGCTCCCTGCTGCGCCACTTCCCCATGCCAGCGGCAGTTCTTGAAGC  
 TCGGGGGGCTGCAGGTCTTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG  
 CGCGTGCTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCCGAGGAGGAGGCTGA  
 GCTGACCCAGGAGATGTCCCAGAGAAGCTGCAGCAGTATGCCAGGTACACCTCCTGCCAG  
 GCCTGTGGGAACAGGGCTGGTGCGAGATCACGGCCCACCTCCTGGCGCTGCCCGAGCATGAT  
 GCGCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGTACCG  
 TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA  
 GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC  
 AGCTTGCTGAAGGAGCTGAGAT**TGA**GGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA  
 GGCTGAGGGGTGCCAGCTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCT  
 TGCCATTAAATGGAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AA

**FIGURE 218**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL  
 DAEVLEVFHPTHEWQALPQGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN  
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV  
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF  
 VLGAAFSSNPVKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL  
 GGLQVLRRTLQVEKGTEVLAVRVVTTLLYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG  
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCDRYRQDPQLGRTLASLQAEYQVLAS  
 LELQDGEDEGYFQELLGSVNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340

**FIGURE 219**

TTCGGCTTCGGTAGAGGAAGTGGCGGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCC  
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCTCGTGGGGTCGCGTTGCCACCCCA  
 CGCGGACTCCCCAGCTGGCGCGCCCTCCCATTTGCCGTGCTCGTTCAGGCCCCCCACCCCC  
 TTCCCACCTGACAGCC**ATG**GGGGCTGCGGTGTTTTTCGGCTGCATTTTCGCGCTTCGGC  
 CCGGCCTTCGCGCTTTCTTGATCACTGTGGCTGGGACCGCTTCGCGTTATCATCTGGT  
 CGCAGGGGCATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTATCTTGG  
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCT  
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCCTACTACAAGCTGCTAAGAAGGCAGA  
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT  
 ATGTTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT  
 GATGCACTTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCTGACTTC  
 AGCCTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG  
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCTGGTGGTTGGGAGTCACCTACTGACATCG  
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT  
 TTCCATGGGGCTCTGGGCCTTATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCC  
 TCTTGTGTAAGGAC**TGA**CTACCTGGACTGATCGCTGACAGATCCACCTGCCTGTCCACTG  
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATTCTGTCTCCTTCTCGTC  
 GGTCTACCCCACTACCTCCAGGGTTTGTCTTTGTCTTTGTGACCGTTAGTCTCTAAGCTT  
 TACCAGGAGCAGCCTGGGTTACGCCAGTCACTGACTGGTGGGTTTGAATCTGCACTTATCCC  
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGAGTGTCTGCTCTCAC  
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGCGAGCCGACGCGAGAGGACAGTCGGGTGAT  
 GGTGTATCTGCCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC  
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGACG  
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAATTAATGGAGGCTCAA  
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC  
 AGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCTAAACTGCCTTTTTTCTTTTTT  
 GAGGTGGGGGGAGGGAGGAGGTATATGGAACCTTCTAACCTCCTTGGGCTATATTTCTC  
 TCCTCGAGTTGTCTCATGGCTGGGCTCATTTTCGGTCCCTTCTCCTTGGTCCAGACCTT  
 GGGGAAAGGAAGGATGATGTTTGGGAAGTGGCATTACTGGAACATAATGGTTTTAACTC  
 CCTTAACCCACGATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGC  
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGG  
 GAGATTTTTTGTAGTTTTTAATGGGGGTGGGAGGGGGGGGAGGTTTTCTATAAAGCTGT  
 ATCATTTTCTGCTAGGGGTGGAGTGCCCATCCTTTTAAATCAAGGTGATTGTGATTGTGACT  
 AATAAAAAAGATTTGTAAAAA  
 AA  
 AA

220/330

**FIGURE 220**

MGA AVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR  
SDARLQYGLLIFGA AVSVLLQE VFRFAYYKLLKKADEGLASLSE DGRSPISIRQMAYVSGLS  
FGIISGVFSVINILADALGPGVVG IHGDS PYYFLTSAFLTAAIILLHTFWGVVFFDACERRR  
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSL LCKD

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**FIGURE 221**

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGTTGAGTGAGGACGGAAGATCAACCCA  
TTTCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGNT  
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC  
TCACCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

**FIGURE 222**

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTGGTGCTGCTGTNTCTG  
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG  
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN  
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTTNTCTGTTATCAATATTTGGNTGATGCAN  
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTAATTCTGAATTCAGCCTTT  
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGATGCCTGTGA  
GAGGAG

0903725-1501

**FIGURE 223**

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTCCCTTTCCCCG  
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC  
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCACNTG  
ACCAGCCATGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTCGGCCCGGCCTTCG  
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTGGTCGCAGGGGCA  
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGAC  
CGACCGGTCAGATGCCCGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTCC  
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA  
GCATCGCTGAGTGAGGACGGAAGATACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG  
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG  
GCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

**FIGURE 224**

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTTCCCNNTTCCCGGGG  
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC  
CAGNTGGCGCGCCCTCCCATTTGCCCTGTCCTGGTCAGGCCCCACCCCTTCCACCTGA  
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTCGCGTTTCGGGCCCCGGCCTTC  
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGC  
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCTCTGTGGTCTGGTTTCATCTTGGTCCATGTGA  
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCTCCTGATTTTTGGTGCTGCTGTCTCTGTC  
CTTCTACAGGAGGTGTTCCGCTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT  
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG  
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT  
GGGCCAGGTGTGGTTGGGATCCATGGAGAC



**FIGURE 225**

GCCCCAGGGAGCAGTGGGTGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAG  
 TGGCCAGGAAGGCACAGGCCCTGAGAACTGCGGCTGAGCTGGGAGCAATCCCCACCCCC  
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAGGAGAGG  
 TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT  
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT  
 CTTGTGGTTCCTCTCTACCTGGGGAATAAGGTGCAGCGGCC**ATGG**GCTACAGCAAGACCCC  
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT  
 CTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA  
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA  
 ATGGATCCGACTGCGATATGCACACCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC  
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCAGGCCGCCCACTGCGAG  
 GAAGAAAGTTTTAGAGTCCGTCTCGGCCACTACTCCCTGTCAACAGTTTATGAATCTGGGC  
 AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT  
 AACGACCTCATGCTCATAACTGAACAGAAGAATTCGTCCCACTAAAGATGTCAGACCCAT  
 CAACGCTCTCCTCTCATTGTCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGACAA  
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGT  
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA  
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC  
 TGCAGGGACTCGTGTCTGGGGAGATTACCTTGTGCCCGGCCAACAGACCGGGTGTCTAC  
 ACGAACCTCTGCAAGTTACCAAGTGATCCAGGAAACCATCCAGGCCAACTCCT**TGA**GTGTCAT  
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG  
 ACCCTCATTCTCTCCAGAGATGTTGAGAATGTTTATCTCTCCAGCCCCTGACCCCATGTCT  
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCTGG  
 GAACAATTTCCAAAAGTGTCCAGGGCGGGGTGCGTCTCAATCTCCCTGGGGCACTTTCAT  
 CCTCAAGCTCAGGGCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA  
 CTGAGAAGTGGAATAAAAAA

**FIGURE 226**

MATARPPMMWVLCALITALLGVTEHVLANNNDVSCDHPSENTVPSSGNQDLGAGAGEDARSDD  
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS  
PVYESGQQMFQGVKSI PHPGYSHPGHSNDLMLIKLNRRI RPTKDVRPINVSSHCP SAGTKCL  
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGDSGGP  
VVCNGSLQGLVSWG DYPCARPNRPGVYTNLCKFTKWIQETIQANS

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**FIGURE 227**

**ATG**GTCAACGACCCGGTGGAAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCCGCGCGA  
 CAAGCGCGACGCGCCGAGCTCGGGTACGTGCTGTGCACCGTGCTGCTGGCCCTGGCTGTGC  
 TGCTGGCTGTAGCTGTACACGGTGCCTGCTCTTCTGAAACACACGCCACGCGCGGGGCACG  
 GCGGCCCCACCTGTCTGTACGACTGGGGTGCAGCGCCAAACAGCGCCCTGGTCACTGTGGA  
 AAGGGCGGACAGCTCGCACCTCAGCATCTCATTGACCCGGCTGCCCGACCTCACCAGACA  
 GCTTCGACACGCTGGAGAGCGCCAGGCCCTGGTGTGTCAGGCGCTGACAGAGCAGCAGGCG  
 CAGCCACGGCTGTGTGGCGACACAGGAGCAGGAGCTGCTGGACACGCTGGCCGACCAAGCTGCC  
 CCGCTGTCTGGCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG  
 GCACGCTGGGCGCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGCGCCCTCATCGAGCTTCTC  
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTGAGCGACATCTTGGATGCCCT  
 GCAGAGGGACCGGGGGCTGGGCCGGCCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC  
 GGGGAACCGGCCCGGGGGCTGTGCCACTGGCTCCCGGCCCGAGACTGTCTGGACGTCTCTC  
 CTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTCTTCCACCCACTACCCGGCGGGCTT  
 CAGGTGTATCTGTGACATGCGCAGGACGGCGGGCTGGACGGTGTTCAGCGCCGGGAGG  
 ACGGCTCCGTGAACCTTCTCCGGGGCTGGGACGCTACCGAGACGGCTTGGCAGGCTCAC  
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACAGGCTGCCTACGAGCT  
 GCACGTGGACCTGGAGACTTTGAGAATGGCACGGCTATGCCGCTACGGGAGCTTCGGG  
 TGGGCTTGTCTCCGTGGACCTTGAGGAAGACGGGTACCGCTCACCGTGGCTGACTATTC  
 GGCACTCGAGGCGACTCCCTCTGAAGCACAGCGGCTAGGTTTACCACCAAGGACCGTGA  
 CAGCGACCATTCAGAGAACAACCTGTGCCGCTTCTACCGCGGTGCTGGTGGTACCGCACT  
 GCCACAGCTCCAACCTCAATGGGCGTACTCTGCCGGTGGCACGCTCTATGCGGACGGC  
 GTGGAGTGGTCTCTTGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCGC  
 GCGGTCGCGGAGACCGCT**TAG**ACTGGTGCACCTTGTCTTGGCCCTGCTGGTCTGCTCGC  
 CCCATCCCCGACCCACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCTTGGCGGAC  
 CCACCTCTCAGTAGGGAGGGGCGGGCCATCCCTGACACGACTCCCTGGCGCGGTGAAGT  
 CACACATCGCCTTCTCGCGCTCCCGACCCCTCAATTGGCAGCTCACTGATCTCTTGGCTC  
 TGCTGTATGGGGCTGGCAAACCTTGACGACCCCACTCTGCTGCTGGCCCACTGTGACTCGG  
 TGCTGTTTGGCTCCCTGGCCAGGATGGTGGAGTCTGCCCGAGGACCCCTTGGCCCTGCC  
 GGCCAAATACGCGGAATATGGGGACAGAGAGCAGGGGGCAGACAGCACCCTGGAGTCTCT  
 CTAGCAGATCTGGGGAATGTGAGGTCTCTGTGAGGTGAGGTCTGAGGCCAGTATCTCCAG  
 CCTCCCAATGCGCAACCCCAACCCGTTTCCCTGGTGCCAGAGAACCCACCTCTCCCCAA  
 GGGCTCAGCTGTGCTTGGGGCTGGGTGGCCCATCTTACAGGGCCTGAGGTGAGGATGGG  
 GAGCTGTGCTTTGGGGACCCACGCTCCAAGGCTGAGACCAATTCCCTGGAGGCCACCCAC  
 CCTGTGCCCGCGAGGCTGGGGCTGTCAGTCTCTTACCTGCTGTGCCACACTGCTCTCTG  
 TCTCAAATGAGGCCCAACCCATCCCCACCCAGCTCCCGGCGTCTCTTACCTGGGGAGC  
 CGGGCTGCCATCCCAATTCTCTGCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT  
 GCACTGCGCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGGCTAGGCAAGGCTGGGATGAG  
 GCTTGTACACGCCCAACCAACCAATTTCCAGGGACTCCAGGCTCTGAGGCTCCCGAGGAG  
 GCTTGGGGGTGATGACCCCTTCCCTGAGGTGCTGTCTCATGAGGAGGCCAACCTTGGC  
 ATTGACCGTGGCACCTGGACCCAGGCCAGGCCCGGCCCGGCGAGTGGTCAAGGGACAGGGA  
 CCACCTCAGCGGGCAATGGGGTGGGGGAGCTGGGGACCAAGGACCAACCTGAGGACA  
 TTTCTTGTGTAATCTCCCAACACCCAGCACCTGTCTATCCCACTCTTGTGTGACACA  
 CTCAGAGGTGAGACCCCGAGGCTCCAGGACCAAGGACCAAGGCGAGGCTGGAGCGGG  
 TCTCTAGCTGTCTGCTCAGCAGCCCTGGACCCGCGTGCCTTACGTGAGGCCAGATGACAGG  
 CGGCTTTTCAAGGCCTCTGATGGGGGCTCCGAAAGGGCTGGATCAGCTTGGGGAGCT  
 GCTAGCAGCTCTCTCTGGGAGGAGGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA  
 GGTGCTAGGGGTGTGGGGTTCGGTTCTCCCTCCCACTGAAGTTTGTGCTTAAAA  
 AACAATAAATTTGACTTGGCACCACTGGGGGTGGTGGGAGAGGCCGTGTGACCTGGCTCTC  
 GTGCCAGTGCCACCAAGGTATCCACATGCGCAG

**FIGURE 228**

MVNDRWKTMGGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVTGAFLFNHHAHAPGT  
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA  
QPRLVGDQEQELLDTLADQLPRLLARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL  
SESQGHMAHLVNSVDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL  
LSGQQDDGVYSVFPFTHYPAGFQVYCDMRDGGGWTVFQRREDGSVNFRRGWDAYRDGFGRLT  
GEHWLGLKRIHALTTQAAAYELHVDLEDFENGTAARYGSFGVGLFSVDPEEDGYPLTVADYS  
GTAGDSLKKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG  
VEWSSWTGWQYSLKFSEMKIRPVREDR

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**FIGURE 229**

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT  
 TGCTTCTCTGAAGTACAGTACAGTAGCCGCGGCCAGGGCAATCCGACCACATTTCACTCT  
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCAGGAGGACATGCTGGATGATG  
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC  
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCCTGCTGAC  
 TTTGTGCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACC  
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC  
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC  
 TGAAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG  
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAGACAGCAAAAGTTGGGAG  
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAACAAGAAGA  
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTAGTTTTTCTACTCTTATTGGACAGGGCTTT  
 TCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAAGT  
 TTCCATATTATAATAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG  
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA  
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTGCC  
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT  
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTTCTCGTG  
 TTTCTGTTCAGGATCACCAGCATTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA  
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCTATCTGCCTTCTTG  
 GCTTAGAGATAAAGTTTAGTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTAT  
 GTCTTCTTACACTTGGTGGAAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC  
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCAGATTGTACC  
 AGCAAATACACAAGGAATCTTTTTGTTGTTTCAGTTCATACTAGTCCCTTCCCAATCCAT  
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG  
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAAGACTCTGATAATTG  
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG  
 AACTACCGTCCCCGATATCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA  
 TCTGCACCTGTAATAGTTTCAGTTCCATTTTCTCCATTGACCCATATTTATACCTTTACG  
 GTACTGAAGATTTAATAATAAATGTAATACTGTGAAAA

MQAKYSSTRDMLDDGDGTTMSLSHQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLL  
IGLAALGLLFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE  
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFASD  
QSYSEFFYSYWTGLLRPDSKGAWHMDGTFPTSELFHIIIDVTSRPSRDCVAILNGMIFSKD  
CKSELKRCVRRAGMVKPESHLVPETLGGDD

**FIGURE 231**

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG  
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG  
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG  
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA  
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA  
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT  
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA  
AGTNTCCTCATNTACTATACACACCACTTCCC

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**FIGURE 232**

GCGGAGCGCAAGAACCCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC  
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGAGGCGGGCCGCCCGCGGGG  
 CCGGAGCCCCTCGGGATCGCGCCCCCTCCCGGGTCCCGCCCCCTCGGAGACTCTCTTGCTGCT  
 CTGGGGGTTTCGCGGGGGCGGGGACCCGCGGTCCGGGCGCC**ATG**CGGGGATCGCTGCTGCTG  
 TCGGTGCTGCGGCCCCGAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTACCCCTGAGCCT  
 GCTCAAGCTCACTGGGTGGAGGAGCGCTGCGGCCAGGCCGCCCAACCTGGAGACTCTG  
 AGCTGCCGCGCGCGGCAACACCAACGCGGCGCGCCGCGCCCAACTCGGTGCAGCCCGGAGCG  
 GAGCGCGAGAAGCCCGGGGCCGCGAAGGCGCGGGGAGAATTGGGAGCCGCGCTTTGCC  
 CTACCACCTGACAGCCCGGCCAGGCGGCCAAAAGGCCGTGAGGACCCGCTACATCAGCA  
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC  
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGGTGGTGTCTCTGAC  
 GGGCGCAGCGGGCGCGCGGGCCCCACCTGGCATGGCAGTGGTGAGCTGGGCGAGGAGCGAC  
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC  
 TGGTTCTTCTGGTGCTGACACCACCTACACCGAGGCGCACGGGCTGGCAGCGCTTAACCTGG  
 CCACCTCAGCCTGGCCCTCCGCGGCCACCTGTACCTGGGCGGGCCCCAGGACTTCATCGGGG  
 GAGAGCCCAACCCCGCCGCTACTGCCACGGAGGCTTTGGGGTGTGCTGTGCGCGCATGCTG  
 CTGCAACAACCTGCGCCCCACCTGGAAGGCTGCCGCAACGACATGTCAGTGCGCGCCCTGA  
 CAGTGGGTGGTGCCTGCATCTTCGATGCCACCGGGGTGGGCTGCACCTGGTGACCAGAGG  
 GGGTGCATATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGCAGGAGGGGACCCCTCAT  
 TTCCGAAGTGGCTTGACAGCCCAACCTGTGCGTGAACCTGTGCACATGTACGAGTGCACAA  
 AGCTTTTCCGCCGAGCTGACTGGAACGCACGTTACAGGAGATCCAGGAGTTACAGTGGGAGA  
 TCCAGAATAACAGCCATCTGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATT  
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA  
 GCACGCTTTTCTCTGCGCCGATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCGGGCTG  
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCCTTACACCCCGGCTTGG  
 CGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGA  
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGAGGCGCGCGGCCCTCACT  
 GCCGAGTGCAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCTGTGCCCTATGTCACT  
 GAGGCCCTCAGCTCTCACTGTGCTGCTGCCCTAGCTGCGGCTGAGCGTGACCTGGGCCCTGG  
 CTCTTTGGAGGCCCTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC  
 TGCTGCTACTGTATGAGCGCGCCAGGCCAGCGCGTGCCCATGCAGATGTCTTCGACCT  
 GTCAAGGCCACGCTGGCAGAGCTGGAGCGCGGTTTCCCGGCTGCCCGGGTGCCATGGCTCAG  
 TGTGACAGACGCCGACCTCACCACTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCGCG  
 TGCACACATGTTCTCTGCTGGCGGGCCAGACACGGTGCTCAGCGCTGACTTCTTCAACCCG  
 TGCCGATGCTGATCTCCGCTGCGGCTGGCAGGCTTCTTTCCCATGCAATTTCCAAGCCTTCCA  
 CCCAGGTGTGGGCCCAACACAAGGGCTTGGGCCCCAGAGCTGGGGCGTGACACTGGCCGCT  
 TTGATCGCCAGGCAGCCAGCGAGGCTGCTTCTACAACCTCGGACTACGTGGCAGCCGCTGGG  
 CGCTGGCGGCAGCCTCAGAACAGAAGAGGAGCTGCTGGAGCGCTGGATGTGTACGAGCT  
 GTTCTCTCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT  
 ACCGGGCCAGAGCTGCGAGCGAGGCTCAGTGAGGACCTGTACACCCGCTGCCCTCAGAGC  
 GTGCTTGGAGGCTCTGGCTTCCGAAACCCAGCTGGCCATGCTACTTTGAACAGGAGCAGGG  
 CAACAGCACT**GCA**CCCCACCTGTCCCGTGGGCGCTGGCATGGCCACACCCCACTT  
 CTCCCCAAAACAGAGCCACCTGCCAGCCTCGCTGGGCGAGGCTGGCCGTAGCCAGACCC  
 AAGCTGGCCCACTGGTCCCCCTCTGGCTCTGTGGTCCCTGGGCTCTGCACAAGCACTGGG  
 GGACGTGCCCCAGAGCCACCCACTTCTCATCCCAACCCAGTTTCCCTGCCCCCTGACGCT  
 GCTGATTCCGGCTGTGGCCCTCACGATTATTATGCAGTACAGTGTGCTGACGCCAGCCCTGG  
 CTCTGGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTGGGGAAGGAGGAGCTGAGGAGGG  
 GCATCTCCCAACTTCTCCCTTTTGGACCGTGGCAAGCTCCCTGCTTTAATAAACTGGCCA  
 AGTGTGAAAAA



**FIGURE 233**

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP  
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQLLVAVL  
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL  
QHGGDDFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG  
VLLSRMLLQQLRPHLEGCRNDIVSARPDWLGRCLDATGVGCTGDHEGVHYSHLELSPGEP  
VQEGDPHFRSALTAPVRDPVHMYQLHKAFARAELETTYQEIQELQWEIQNTSHLAVDGDRA  
AAWPVGI PAPS RPAS RFVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTAEELN  
RRYHPALRLKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGRRPLTRRVQLLRPLSRVEI  
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA  
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL  
TPDFLNRCRMHAISGWQAFPPMHFQAFHPGVAPPQGGPPPELGRDTGRFRDQAASEACFYNS  
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTC SARLSEDL  
YHRCLQSVLEGLGSRTQLAMLLFEQE QGNST

**FIGURE 234**

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT  
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCCTAGTGGAGAAAAGGAGT  
 AGCTATTAGCCAATTTCGGCAGGGCCCGCTTTTGAAGCTTGATTTCCTTTGAAGATGAAAG  
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA  
 CTGTATCCACCCAAATGTCACCGATTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA  
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG  
 AGGGTTGCTCAACGCCCCGCCTCATTGGAACCAAAATCAGATCTGGGACCTATATAGCGTG  
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT  
 TTCCCCGCCCTGAGACCTGCAGCACCATCTGTCA**ATG**GCGGCTGGGCTGTTTGGTTTGAGC  
 GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCGCTCCGCTGGGA  
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGGCCCCAGAAC  
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCA  
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTGTGGAACATGCGACTTGTCTTCTT  
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA  
 GGATGAAAGAGTGGTCCCGCCGCAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC  
 CTTCCCATCATGGAATCCAATGCTTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**  
**A**CCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC  
 CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

**FIGURE 235**

MAAGLFGLSARLLAAAATRG LPAARVRWESSFSRTVVAPS AVAGKRPPEPTTPWQEDPEPE  
DENLYEKNPDSHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER  
LVKYREANGLPIMESNCFDPSKIQLPEDE

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**FIGURE 236**

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC  
TCCCGGCCGCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT  
GTGGCGGGAAAGCGGCCCCAGAACCGACACACCGTGGCAAGAGGACCCAGAACCCGAGGA  
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG  
TCTGGAACATGCGACTTGCTCTTCTTTTGGCGTCTCCATCATCTGTCCCTTGGCAGCACC  
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCT  
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAC TGCTTCGACCCAGCA  
AGATCCAG

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GC GCGGGCGCT**TATG**CCGCTTGCTCTGCTCGTCCGTTGCTCCTGGGGCCCGCGGGCTGGTGCCCT  
TGACAAGACCCCAACGCCAGACGCTCGGGAGGAACTGTGATCAACCCCGCTGCCCTTCGGGG  
ACGTAGCGGCCACATTCCAGTTTCCGACGCGGCTGGGAATTGAGAGCTTACGGGGGAAAGGATG  
TCCATTACAGGCTCTTTTCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTTCTACGGACA  
GCTGCACCTGTCTTACACAAAGGCTTTTGAGGAGCCGATCTGGGGGACCCCTTCTGTG  
AGGCCCATCAGTGCAGAGTGTGGGCTTGCTGGTTCCAAAGACACTGTCACTGATGTGGATAAA  
TCTTGGAAAGGAGCTCAGTAATGTCTCTCAGGATCTTCTCGGCCCTCTCAACTTATCTGCA  
CTCCACCAACAGCTCACTCCCACTGCCCTCTTCAAACCCCTGGGTTGGCCAAATGACACTG  
ACCATACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC  
CTCTGGGAAGAAGACTTTGGCCCTGTAGTTTCCAAGGACGATCTCTGTGTGCTGTGAAGGCAGA  
TCGTTGTGTTCCACACCGACTACCCTCCAGGACGTGACATCTCGCCCTGTTTGCAGAAATG  
CACGCTGTATAGCATCTCTCTGGGAGCTGAGGCGAGACCTCTGAGTTGTATTGTATGCTCTT  
ACACGCGGGCAGGGAAAGAACACTGGTCTCCTTCCGAGTGTTCTCCCGAACCCCTCAGGA  
GCCCTGCCCTGGCTTCCAGAGAGCCGAGTGTATGTGACATCAACCACTACAACCGAGACA  
ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATACAGGACGCTCATCTTAGGACAT  
CGGAAGACCTATGCCATAGACTGTGCTTGTACACCGCCATGATCAACAACCTCTCGAAACCT  
CAACATCCAGCTCAAGTGGAAAGACCCCCAGAGAATGAGGCCCCCCAGTGCCCTTCTCTGC  
ATGCCACGCGGTACGTGAGTGCTATGGGCTGCAAGAGGGGAGCTGAGCACACCTGTGCTTAC  
AACACCCACCAATACCGGGCTTCCCGGCTGCTGTGCTGGACACCGGTACCTGGTATCTGGC  
GCTGTATGTGCACACCCTACCATCACTCCCAAGGCGAAGGAGAACAAACAAAGTTACATCTC  
ACTACAGCGCTGCCAGGACCGGCTGCAACCCAGGCTCTGGAGATGCTGATTCACTGCTCCG  
GCCAATCAGTACCAAGGTTTCCATCGAGTTTGAAGCGGGCGCTGCTGAAGTGGACCGAGTA  
CAGCGCAGATCTTAACATGGCTTCTATGTACGCGCATCTGTCTCCAGCGCCCTGTGGCCCA  
GCTGGTAGACACCAAGCAGGTGAGCTGGGAAGAGAGTCCCTCTTCAACAAGCCTGTGTCCCA  
GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC  
GACACCGGCACTCAGCATGCCCTACACGTGCTGCTGCTCACTGCTGACCTGTGGTGCCCTGTG  
GCTACGGCTCTCTTCTACAATCTCTCACCGCAACCTTCCATCTGAGGAGGCCCGCAGAGT  
GGCTCTGGCCACGCGCTGGCCAAACCTTATCCGGCGCGCGAGGTTGTCGCCCACTCT**TGA**T  
CTTGCCCTTTCCAGGCTCGAGCTGCCGCTTCTCTGGGAGGGGAGCCCAAGGCTGTT  
TCTGCCACTTGTCTCTCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCCAGGTACAGGC  
CTACAGCTGTGTTTCCAGTACAGGACGACGAGCAAGCAATGTGGCAATTGAATTTGAATTTAA  
CTTAGAAATTAATTCTCTCACTGCTAGTGGCCACTCTATATTGAGTGTCTTAATGAAGTAA  
AGTGTGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACCACAGAAAGTTC  
GGCTGGACAGCACTGGCCAAAGGTTGATGGGTTGTGTACACAGTATATGCTACTGTGTAGTGG  
TGGAGTTTACTGTTTGTGAATAAAAAACCGCTGTTTCCGTGGAAAAAATAAAAAA

**FIGURE 238**

MPLALLVLLLLGPGGWCLAEP PRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY  
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDVTVDVDSWK  
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK  
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSSISWELRQTLSVVFDAFITG  
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT  
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH  
PYRAFPVLLLDTPVWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS  
VTKVSIOFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD  
GSNYFVRLYTEPLLVLNLPDPFSMPYNVICLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLA  
KRLANLIRRARGVPPL

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**FIGURE 239**

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCTGGTGG  
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTGCCAGCTGACAACGTACGC  
TGCTTCAAGTCCGATCCTCCCAAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG  
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA  
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC  
TCCTCCTCTACCAGGTGTCCTCAGAAAATGATGCTGGGTCTTTCTACCTCTGGGGGTCACTC  
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGAATATGGAAGAAGCAATACCCAACC  
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG  
TCCAGACCCCAGGGACGGTACTTCCCTCTCTACCTGGTGTCTCTCCCTAATGCTCATGAAT  
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC  
TGCAATGTGTGATCACAGCTAGAAGGCACGTGCAGAGAAGAGAACTGGTCCTCACCAGATG  
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAAGTGAAGAAATAAATAT  
TTGCTGTTTATAATCCAA

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**FIGURE 240**

MGSSSFVLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC  
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

**Signal sequence:**

amino acids 1-19

**N-myristoylation sites:**

amino acids 23-29, 27-33, 32-38, 102-108

**WAP-type 'four-disulfide core' domain signature:**

amino acids 49-63

0998725-112001



**FIGURE 241**

AAACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACCTTCTGGCCAGG  
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC  
 TCTAGAACC CGACCCACCACCA**atg**AGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAAGG  
 CGTCCAGTGGTCCTTGCTTCTGGCTGTCTGGTCTTCTTTCTCTGCCCTTGCCCTCTTTTAA  
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTC  
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA  
 TGCAGAGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA  
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGAGGAGAGGAGACAAGGTGCCCCAC  
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAGAGAAAACCATGGTGAACACATGTC  
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC  
 AGGACACAAGACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG  
 GTGTCAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAAGACGCTCATTCCTCAAAGTCA  
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAGGACGAGACAGAAAGGAGTGACCA  
 CAGCAGTCATCCCACTTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCCCTTTCCAG  
 AGCCCCACGACGACAGAGAAACCAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG  
 GGATTTTGAGGAAAATACAGCTTCGAAATAGGAGGCTTCAGACGACTTGCCTGACTCTG  
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCAACCTCACTCTC  
 TTCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCTGGAACACTTTGACCCACC  
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAAGGCTCGTGACACGCTTCCCTCCAG  
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGATCACTCTG  
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA  
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGACCTC  
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT  
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACTTCTTGGAAGGCAC  
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT  
 TCTGGTTACAGGCACAGACCCCAAGGAAGCTTTTCGGGAAGCCTGCACATGGACAGGTACCTG  
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTTGGA  
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC  
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT  
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA  
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACAGCGCTCCTGGTC  
 CCGGAACCTGCCAAAGCCAGAACT**TG**ACCGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC  
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA  
 GCTCCAAAGCCCTTCAGGAGTTCACAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT  
 GGCAAATGGCTAATTGAGGTTCTGAAGTCTTTCAGTACATTGCTGTAGGTCTGAGGCCAGG  
 GATTTTAAATTAATGGGGTGATGGGTGGCCCAATACCAATCTCTGCTGAAAAACACTCTT  
 CCAGTCCAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG  
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAATCTTGAAGGTATTACTTAACCTCACTAC  
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGCTCTATACTTGTCTTG  
 TCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGT  
 GTCCATGGAAAGGCAATAAATTTTCTACAGTGAAAAAAGAAAAA

MRSCLWRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP  
 KSQAPTRARRTTIYAEAPENNALNTQTQPKAHTTGDGRGKEANQAPPEEQDKVPHTAQRAAW  
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQNGGQTRKLTASRTVSEKHQG  
 KAATTAKTLIPKSQHRLAPTGAIVSTRTRQKGVTTAVIPPKEKKPQATPPAPFQSPTTQRN  
 QRLKAANFKSEPRWDFEEKYSFEIGLQTTCPDSVKIKASKSLWLQKFLFLPNLTLFLDSRHF  
 NQSEWDRLEHFAPPFGMELNYSLVQKVVTFRPPVPQQQLLASLPAGSLRCITCAVVGNGG  
 ILNNSHMQEIDSHDYVFLRSGALIKGYEQDVGTRTSFYGFATFSLTQSLILIGNRGFKNPV  
 LGKDVRYLHFLGTRDYEWLEALLMNQTVMSKNLFWFRHRPQAEFREAHMDRYLLHPDFL  
 RYMKNRFLRSKTLDGAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDYTSW  
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

amino acids 1-10

amino acids 11-35

amino acids 36-600

## amino acids 481-496

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

**FIGURE 243**

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG  
GAGCAGCGAGTGGAAATTGTTCCCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT  
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA  
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT  
GTCAGTCCAGTGTGCATGGAGGATAAGTGAAGCAGACCGTACAGGAGCAGCACACCAGGAGCC  
ATGAGAAGTGCCCTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG  
ACAAGAGATTTATTTTTGCAGACAGACTCTTCATAAGTCCTTTGAGTTTGTATGTTGTTG  
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTATCTGTCACTTATTT

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**FIGURE 244**

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT  
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

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**FIGURE 245**

GGGCTGGGCCCCGCCGACGTCCAGCTGGCCGGCTTGCTCCTGCGGTCCCTTCTCTGGGAGG  
 CCCGACCCCGGCCGCGCCAGCCCCACCA**ATG**CCACCCGCGGGGCTCCGCCGGGCCGCGCCG  
 CTCACCGCAATCGCTCTGTTGGTGTGGGGGCTCCCTGGTGCTGGCCGGCGAGGACTGCCT  
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT  
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG  
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT  
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTCTGTTGCTACCTGT  
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC  
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC  
 TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC  
 CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC  
**TGA**GGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT  
 CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA  
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAACTAGA  
 ACTATGAGGGGTTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG  
 GAGATGACAGCCTGGGTACAGTGCCCTGTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG  
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGT  
 TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGCTGCCCACTGGCCACATCTCTGGCCTG  
 CTAGATTAAAGCTGTAAAGACAAA

**FIGURE 246**

MPPAGLRRAAPLTAIALLLVGLAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYC  
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSP  
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPSPGPAPQYPLYPAGPVPVYNPAAPPP  
YMPQPQPSYPGA

**Transmembrane Domains:**

amino acids 10-28, 85-110

**N-glycosylation Site:**

amino acids 38-41

**N-myristoylation Sites:**

amino acids 5-10, 88-93

000072512000

**FIGURE 247**

GGGGGAGCTAGGCGGGCGGCAGTGGTGGTGGCGGCGCGCAAGGGTGAGGGCGGCCCCAGAA  
 CCCCAGGTAGGTAGAGCAAGAAAGATGGTGTCTGCCCCCTCAAATGGTCCCTTGCAACCATG  
 TCATTTCTACTTTTCTCACTGTTGGCTCTCTTAACGTGTCCACTGCTTCATGGTGTCCAGAG  
 CACTGAAGCATCTCCAAACGCTAGTGATGGGACACCATTTCCTTGAAATAAAAATACGACTTC  
 CTGAGTACGCTCATCCAGTTTCAATATGATCTCTTGATCCATGCAAACTTTACACGGTGACC  
 TTCTGGGGAACACGAAAGTAGAAATCACAGCCAGTCAGCCCCACAGACCATTCATCTGCA  
 TAGTCCACAGCTGCAGATATCTAGGGCCACCTCAGGAAGGAGCTGGAGAGAGGCTATCGG  
 AAGAACCCCTGCGAGCTCTGGAACACCCCTCAGGAGCAAAATGCATGTCTGGCTCCCGAG  
 CCCCCTCTGTCTGGCTCCCCTACACAGTTGTCAATCACTATGCTGGCAATCTTTGGGAGAC  
 TTTCCACGGATTTCACAAAGCACCTACAGAACCAAGGAAGGGGAAGCTGAGGATACAGCAT  
 AAACCAAAATTTGAGCCACTGCAGCTAGAATGGCTTTCCCTGCTTTGATGAACCTGCCTTC  
 AAAGCAAGTTTCTCAATCAAATTAAGAGAGAGCCAGGCGACCTAGCCATCTCCAATATGCC  
 ATTTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGA  
 AGATGAGCACCTATCTGTGTGGCTTCATCATTTTCAGATTTTGAGTCTGTGACGCAAGATAACC  
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGGCCAGACAAGATAAATCAAGCAGATTATGC  
 ACTGGATGCTGCGGTGACTCTCTAGAATTTTATGAGGATTATTTTCAGCATACCGTATCCCC  
 TACCCAAACAAAGATCTTGTCTGCTATTCCCGACTTCAGTCTGGTGTATGGAAAACTGGGGA  
 TCACACACATATAGAGAATCTGCTCTGTTGTTGATGCAGAAAGATCTCTTCATCAAGATAA  
 GCTTTGGCACTAGAGTGTGTCGCTGAACTGGCCACCAAGCTGGTTTGGGAACCTGGTGA  
 CTATGGAAATGGTGAATGATCTTTGGCTAAATGAAGGATTGCCAAATTTATGGAGTTTGTG  
 TCTGTGAGTGTGACCACTGTTGAACTGAAAGTTGGAGATTATTTCTTTGGCAATGTTTGA  
 CGCAATGGAGTGTAGATGCTTTAAATTCCTCACACCTGTGTACACCTGTGGAAATCTCTG  
 CTCAGATCCGGGAGATGTTTGATGATGTTTCTTATGATAAGGGAGCTGTATTCTGATATG  
 CTAAGGAGATGATCTTAGCGCTGACGCATTAAAGAGTGTATTGTACAGTATCTCCAGAAGCA  
 TAGCTATAAAATACAAAAACGAGGACCTGTGGGATAGTATGGCAAGATTGTGCCCTACAG  
 ATGGTGTAAAGGGATGGATGGCTTTTGCTCTAGAAGTCAACATTCATCTTCATCTCCAT  
 TGGCATCAGGAAGGGTGGATGTGAAACCATGATGAACACTTGGACACTTGGAGAGGGGTTT  
 TCCCTTAATAACCATCACAGTGAAGGGGAGGAATGTACACATGAAGCAAGAGCACTACATCA  
 AGGCTCTGACGGGCCCCCGACACTGGGTACCTGTGGCATGTTCATTGACATTCATCAG  
 AGCAAAATCCAACATGGCTCATCGATTTTGTCAAAACAAAAACAGATGTGCTCATCTCTCC  
 AGAAGAGGTTGGAATGGATCAAATTTAATGTGGGCATGAATGGCTATTACATTTGCTATACG  
 AGATGATGGAATGGGACTCTTTGACTGGCCCTTTTAAAGGAACACACAGCAGTCAAGCAT  
 AATGATCGGGCAAGTCTCATTAACAATGCATTCAGCTCGTCAGCATTGGGAAGCTGTCCAT  
 TGAAGAGGCCCTGGATTTCCTGTACTTGAACATGAAACTGAAATTTAGCCCGTGTTC  
 AAGCTTTGAATGAGCTGATTCTCTATGATAAGTTAATGGAGAAAAGAGATGATGAATGAAGT  
 GAAACTCAATCAAGGCCCTCTCATCAGGCTGCTAAGGGACCTCATTTGATAAGCAGACATG  
 GACAGACAGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACACTACTCTCTCGCTGTG  
 TGCACAACTATCAGCGCTGCGTACAGAGGCGAGAAGGCTATTTTCAGAAAGTGGGAAGGAATCC  
 AATTGGAACCTTTGAGCTGCTCTGCGAGTGAACCTTTGGCAGTGTCTTGTGGGGGCCAGAG  
 CACAGAGAGGCTGGGATTTTCTTTATAGTAAATACAGTTCCTTTGTCCAGTACTGAGAAAA  
 AGCAAAATGAAATTTGCCCTCTGCAGAACCCAAATAAGGAAAAGCTTCAATGGCTACTAGAT  
 GAAAGCTTTAAGGGAGATAAAATAAAACCTCAGGAGTTTCCACAAATCTTTACACTCATGG  
 CAGGAACCCAGTAGGATACCACTGGCCTGGCAATTTCTGAGGAAAACCTGGAACAACTTG  
 TACAAAAGTTTGAATCTTGCTCATCTTCCATAGCCACATGGTAATGGGTACAACAAATCAA  
 TTTCTCCACAGAACCGGCTTGAAGAGGTAAAGGATTCTTCAAGCTCTTTGAACGATGTAA  
 TTTCTCAGCTCGGTTGTGTCCAACAGACAATGAAACCATGGAAGAAACATCGGTTGGATGG  
 ATAGAATTTTGATAAACTCAGAGTGTGGCTGCAAAGTGAAAGCTTGAACGATGTAA  
 TTTCTCCCTTGTCCCGGTTCTGTTATCTCTAATCACCACATTTTGTGAGTGTATTTTCAA  
 ACTAGAGATGGCTGTTTGGCTCCAACCTGGAGATACCTTTTCCCTTCAACTCATTTTGTGA  
 CTATCCCTGTGAAAGAAATAGCTGTTAGTTTTCATGAATGGGCTTTTTCATGAATGGGCTA  
 TCGCATACCATGTGTTTGTTCATCACAGGTGTGCCCCTGCACAGTAAACCAAGTGTGGGT  
 TCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAA

09989725.1.1201

**FIGURE 248**

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH  
 YDLLIHANLTTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEELQVLE  
 HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA  
 ARMAFFPCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSLYLVA  
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLFEFYEDYFSIPYPLPKQDLAA  
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELAHQWFGNLVTMEWNNDL  
 WLNIEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD  
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGMDG  
 FCSRSQHSSSSSHWHQEGVDVKMTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD  
 TGYLWHVPLTFITSKSNMVRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL  
 TGLLKGTHTAVSSNDRASLINNAFQLVSI GKLSIEKALDLSLYLKHETEIMPVFQGLNELIP  
 MYKLMKMRDMNEVETQFKAFLIRLLRDLIDKQWTDEGSVSEQMLRSELLLLACVHNYQPCV  
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTESKQIEFALC  
 RTQNKEKLQWLLDESFKGDKIKTQEFPPQILT LIGRNPVGYPYLAQWFLRKNWNKLQKFELGS  
 SSIAHVMVGTNNQFSTRRLREEVKGFSSSLKENGSQLRCVQQTIETIENIGWMDKNFDKIR  
 VWLQSEKLERM

**Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360



**FIGURE 249**

CAGCCACAGACGGGTCATAGCGCGGTATTACTGCTGCCCTCCTGGGGTTTCATCCTCCCAC  
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
 GACCTACCCCGGCAATGGACCCCTAAGAACACACAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCTCAAGGGCTGCACGG  
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCTGATC  
 TCCTACACCTTCGTGTGCCGCGAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG  
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACTGTTATGAT  
 GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA  
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGACCACCATTATGACACACGGAAC  
 TTGGCTCAAGAACCCTGATTTGGACCACATCGAATACCGAGATGTGCAGGTTGGGGCAGGT  
 GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG  
 GCTGCAGCACTGTTGGGGCTCAAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
 GTGCTTGTGGCCTCCTATACCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT  
 CTACCTGTGTGACGCCCCCTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
 GCGCCCACTCATTGTTATGATGGGTACATTTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT  
 GAGCATTACAGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGTAACCACACCAGACAAATCG  
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
 GTGGGGAGTGGTTTGCCCTTCTGCTTAACTCTATTACCCCCACGATTCTTACCGCTGCTGA  
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTT  
 CCATTCTGTCCATGAATCATCTTCCACACACAATCATTATATCTACTCACCTAACAGCA  
 ACACTGGGGAGAGCCTGGAGCATCCGACTTGCCCTATGGGAGAGGGACGCTGGAGGAGTG  
 GCTGCATGTATCTGATAATACAGACCTGTCCTTTCA

0909725 11200  
 100211 5226866

**FIGURE 250**

MSAVLLALLGFIPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI  
ESGPQVSLVLSKGCTEAKDQEFVTEHRMGPGSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCFVCLSMEGCLEGTTEEICPKGTTTCYDGLLRLRGGGIFSNLRVQGCMFQPGCN  
LLNGTQEIGFVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL  
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVC  
PSC

CGCAGCGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT  
CAGC**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCTGTCACTGCTG  
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCCTGCTCTGTGCAGATCCTCGTCCCTGG  
CCTCAAAGGGGATGCGGGAGAGAAAGGGAGACAAAGGCGCCCCGGACGGCCTGGAAGAGTCG  
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGTCTGTAT  
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC  
TGGTCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG  
AGATGGACAACCAAGTCTCTCAGCTGACCAGCGAGCTCAAGTTTCATCAAGAATGCTGTGCC  
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA  
CGCCCAAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCA  
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC  
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAAG  
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCTGGAGATGGTGGCCT  
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTCTGATGTGAGTTGACAAG  
GAGAACATG**TGA**GCCTCAGGCTGGGGCTGCCATTGGGGGCCCAATGTCCTCGAGGGTT  
GGCAGGGACAGAGCCCAACCATGGTGCCAGCCAGGAGAGCTGTCCCTCTGTGAAGGGTGGAG  
GCTCACTGAGTAGAGGGGTGTTGTCTTAACCTGAGAAATGGCCATGCTTAAAGAGAAAATG  
AAAGTGTCTCTGGGGTGTCTGTCTGAGAAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA  
ATGTCTATTATGTAATTATTACCCAGAATTGCTCTCCATAAAGCTTGTGCCCTTTGTCCAAGC  
TATACAATAAAATCTTTAAGTAGTGAGTAGTTAAGTCCAAAAA

MRGNLALVGLISLAFSLSPSGHPQFAGDDACSVQILVPLGLKGDAKEGDKGAPGRPRGRVG  
PTGEKGMGMGDKGQKGSVGRHGKIGPIGSKGEKDSGDTGPPGPNGEPLGPCESQLRKATGE  
MDNQVSQLTSELKFIKNVAGREKTESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN  
GLMAAYLAQAGLARVFIGINLKEKAGFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS  
GGWNDVACHTTMYFMCFEDKENM

**FIGURE 253**

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG  
CACCAGTGTGTGAGGGGAGCAGGCAGCGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC  
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT  
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG  
TTCTTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC  
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA  
GGAATCAACATCTCCCAGAAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA  
GGAGCGTCCAGCCAGAGGGAAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCCC  
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC  
TTTTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT  
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCGGGACTCCTGGACTGCATTAGGAAGACCTC  
TTTCCCTGTCCCAATCCCAGGTGCGCAGCTCCTGTACCTTTCTCTTCCCTGTTCTTGT  
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGGAACTGCA  
TAGTGAATATCCCCAACCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT  
CCTACATTAAAAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTTCATATGAA  
AA

**FIGURE 254**

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK  
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFPLPSVRVPRPLHPNQLGSTGK  
SSLGTEEQRPL

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 36-45

**N-myristoylation site.**

amino acids 33-39, 59-65

**Amidation site.**

amino acids 90-94

**Leucine zipper pattern.**

amino acids 43-65

**Tachykinin family signature.**

amino acids 86-92

0000725-12001

**FIGURE 255**

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCGTGTGCCTGCTGTGCC  
 CGCGCTGTCCGCGTCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG  
 GAGCCCTGCCGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCCAGGCTGCCCGTGAGTC  
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTGGGTGGTGTGCATCCCCTTGGGGC  
 TGCTGTTTCTGGTCTGCGGATCCCCAAGGCTACCTCCTGCCCAACGTCACCTCTCTTAGAGGAG  
 CTGCTCAGCAAAATACCAGCACAAACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA  
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT  
 CCAACATGGAGTACATGGTGAAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC  
 CTGGGCCACCAAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGGTGTGATGG  
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTTGTT  
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGACAATCGTCATGCCCTG  
 AAACCTTAGACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG  
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTGTGGAGATGGGGGTCTTGCTACGT  
 TGCCAGGCTGGTCTTGAACCTCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG  
 CTAGGATTATAGGCATGAGTCAACCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA  
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC  
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG  
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCAACCCTGACTTCTC  
 CTTAGCCCGTGTGAGCCTCACTTCCACTTGGAGAGTCCTTCTCGCGTGGTTGCCATGACT  
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCCGCACAGACTGACCTGCCTCCCCAACCCCTAGG  
 CTTTGCTAACCGGGAAGGAGCTAACGGTGACAGAAGACAGCAAGGTCAACCCCTCCCGGGT  
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG  
 TGAAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGCTTCCAGG  
 GTCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGCCATCCGTGAGTATGAATGSGCTT  
 TTTAAACAAACCCACGTCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC  
 CAAGTTAGCCGGGCATGGTGGTGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG  
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGTTGAGCCTGGGAAGTCGAGGCTGC  
 AGTGAGCTGAGATTGCACCATGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAA

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## **FIGURE 256**

MSCVLGGVIFLGLLFLVCGSQGYLLPNVTLEELLSKYQHNEHSRVRRAIPREDKEEILML  
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGR  
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation site.**

amino acids 27-31, 41-45

#### **N-myristoylation site.**

amino acids 126-132, 140-146

#### **Amidation site.**

amino acids 85-89

0000725-12001



**FIGURE 257**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG  
GTCTGGGCTGCCCCTTGTCTCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG  
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC  
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC  
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TGA**CAGCCATTGAAGCCTG  
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCCTGTCTTT  
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTTCGGTATGCTG

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**FIGURE 258**

MSGGLPLVLLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSGTS  
VTLHHARSQHHVCNT

0968723.42004  
T0024.524860

**FIGURE 259**

AATTGTATCTGTGAATGTTAAAACAAACGAAATAAAATAGAAGGAAAAACTTCTGAGTTT  
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAACGTTAGGATTGCAGT  
**TATG**ATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC  
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTGAAAAATGAATGCTTAGTGGATCTG  
TGCCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCCTCCC  
CTCCGATTGTTCTAAAT**TAA**TTGAAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG  
TATGATTCTCAACCATCTTTAGTTGGGAAAGTTCCTTGAAAGCCAATGGAAATACTTTTTTT  
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA  
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT  
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT  
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC  
AGCCTATGTAAGACTACTTTTGTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA  
TCTTCAGATTACTTGATTCAATAAACC AATTATGTTTGT AATTGATTAATAAAAACCAGA  
ATAAAAGTTCATATCTACCC

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**FIGURE 260**

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP

SDCSK

**Important features:**

**Signal peptide:**

amino acids 1-29

098925-12001

**FIGURE 261**

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT  
 GAGAAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGGATGATGGTGCCCTT  
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCCCTTGCAGCTTTTCTGCCCGCCGCTGCTGTAC  
 CCAGGACCCAGCCATGGTGCAATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG  
 AAAAAATGTACCCAAAGCAACGAGGGGCATACATTCAAGAATTCGAAGAGTTCTCAAAAAATATA  
 TCTGTCTAGCTGGGAAGATTTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT  
 GGCACGTGAGAGTTGAACGTGCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGGCTG  
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTGTGCCAAGAGCTGAAGAA  
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC  
 TTTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA  
 ACTCTCCAAAGGTGACTTTATTAATTTGGATCCAGAACAACACTGTTTGGGAATTTGCAAC  
 ATACGGGCATTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTC  
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTCATAACCAAGCAACTT  
 CTAATGAGATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA  
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT  
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTCTCA  
 CRAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTATGGGATACCCCATGCAAGCCAG  
 GATGCTGAAGCCTCATTCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGCCCA  
 GGGCCCTCATCGCATCACTGCATCTATGATCCACTGGGCACATCATGAGGAGGACTTGC  
 CCAACTGTGTTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT  
 AAGCAGCTCTATGCTTGAATGAAGGAAACAGATCATTTACAAACTCCAGACAAAGAGAAA  
 GCTGCCTCTGAAGTAAATGCATTACAGCTGTGAGAAAGAGCATTGGGCTTTGGCAGCTGTC  
 TACGAGCAGTGAAGGCTATAGCCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG  
 GTGTGTAGAAGTGGAAATACGTATGCCTCCTTTCCAAATGTCACTGCCCTTAGGTATCTTC  
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCTATTACTCCCCCAA  
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTGTGTTTACT  
 GCTCCCCAGCATTACTGTAACCTCTGCCCCTCTCCCTCCCAATTAGAGTTGTATGCCAGC  
 CCTAATATTTACCACCTGGCTTTCTCTCCCTGGCCCTTGTCTGAAGCTCTTCCCTCTTTTT  
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAACTATTAAATATTTCTTT  
 CTTTTCTTTCTTTTTTTTGGAGCAAGGTCTCACTATGTTGCCCAGGCTGGTCTCAAACCTC  
 AGAGCTCAAGAGATCCTCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC  
 CACACCTGGCTTAAATACTATTTCTTATTGAGGTTTAACTCTATTTCCCTAGCCCTGTC  
 CTTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAAATATTAACATTTGAATATCGCTT  
 CCAGGTGTGGAGTGTGTCACATCATGAAATCTCGTTTCACTTTTGTGAACATGCACAAG  
 TCTTTACAGCTGTCACTTAGAGTTTAGGTGAGTAACACAATACAAAGTGAAAGATACAGC  
 TAGAAAAATACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAATACGTATGTT  
 TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTCAGCCCTAAAAATATAGTCTGTCC  
 TTTAGCCAGTTTTTCATGCTGCACAAGACCTTTCAATAGGCCCTTCAAATGATAATTCCTCC  
 AGAAAAACAGTCTAAGGGTGAGGACCCCACTCTAGCCTCCTTGTCTGTCTGCTGCTGCT  
 TTCTCTCTTTCTGCTTTAAATTCATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

**FIGURE 262**

MMVALRGASALLVLFLLAFLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYERFQE  
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL  
QEAEEEKKIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTV  
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLEFFHNQATSNEIIKYNLQKRTVED  
RMLLPGGVGRALVYQHSPTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPPTLGVEHSWDT  
PCRSQDAEASFLLCGVLYVVYSTGGQGPHERITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH  
YNPRDKQLYAWNENQIIYKLTQTKRKLPLK

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**FIGURE 263**

GGGCGCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA  
 TGTGCGAGCTCATGGGGCTGTCGGTGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG  
 GTAGCGCGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGCCGCCCGCTTGGCCAAAAGC  
 AAATGGATTTCACCTTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTTC  
 GGAAGGAGAAGCCTCAACAACACAACCTTCAACCACCGCCTCCTGGCTGCAGCTCTGAAGAGC  
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAATACCTGGCTACCTGTGC  
 AGATGATCGCACCATCCGCATCTGGAGCACCAGGACTTCCTGCAGCGAGAGCACCAGCA  
 TGAGAGCCAACGTGGAGCTGGACCACGCCACCTGGTGCCTTCAGCCCTGACTGCAGAGCC  
 TTCATCGTCTGGCTGGCCAACGGGGACACCCCTCCGTGCTCTTCAAGATGACCAAGCGGAGGA  
 TGGGGGTACACCTTCACAGCCACCCAGAGGACTTCCTTAAAAAGCACAGGCGCCTGTCA  
 TCGACATTTGGCATTGTCAACAGGGAAGTTTATCATGACTGCCCTCCAGTGACACCACTGTC  
 CTCATCTGGAGCCTGAAGGGTCAAGTGTGTCTACCATCAACCAACCAGATGAACAACAC  
 ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCTCGTGTGGCTTCACCCAGATGTGA  
 AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGGAGTTCAGGAGGTGGTGCAGCCTTCGAA  
 CTAAGGGCCACTCCGCGGCTGTGCACTCGTTTGTCTTCCAACGACTCACGGAGGATGGC  
 TTCTGTCTCCAAGGATGGTACATGAAACTGTGGGACACAGATGTGGAATACAAGAAGAAGC  
 AGGACCCCTACTTGTCTGAAGACAGGCCGCTTTGAAGAGGCGCGGGTGCCGCGCTGCGCGC  
 CTGGCCCTCTCCCCAACGCCACAGTCTTGGCCTTGGCCAGTGGCAGTAGTATTATCTCTA  
 CAATACCCGGCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGATCGCCA  
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGACCGGGCGGTGCGGGTGT  
 TTTCAACAACCTCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC  
 CTCCAACGAGAGCACCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCTTGA  
 AGAGCTTGGGTGCCCTGAAGAAG**TGA**CTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGAG  
 GGATCTGGCCTCCTCATGGCAGTGTGCCATCTTTCCTCCAGGTGGAAGCCTTTCAGAAGG  
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCCATTTGAACCTACTCTGTCTACTT  
 AGGTCTCTCTTCTTGTCTGGCTGTGACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTTC  
 CTCCAGGCCCACTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG  
 AGGAGAGAGAGAGAGAATGTGATTTTGGCCTGTGGCAGCACATCCTCACACCCAAAGGAG  
 TTTGTAATGTTCCAGAACACCTAGAGAACCTGAGTACTAAGCAGCAGTTTTCGAAGGA  
 TGGGAGACTGGGATAGCTTCCATCACAGAACCTGTGTTCCATCAAAAAGCACTAAGGGATT  
 TCCTTCTGGGCCTCAGTTCTTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTTCGA  
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAGAAAGATGAAAGAGAT  
 AGTACTATTGTCCAATGTCA**TGA**AGTGGTAAAGTGGGAACCAAGTGTGCTTTGAACCCAAA  
 TTAGAAACACATTCCTTGGGAAGGCCAAGTTTTCTGGGACTTGATCATACATTTTATATGGT  
 TGGGACTTCTCTCTCGGAGATGATATCTGTTTAAAGGAGACCTCTTTTCAGTTTCATCAAG  
 TTCATCAGATATTGAGTGCCCACTCTGTGCCAAATAAATATGAGCTGGGGATTAATAAAA  
 AA

**FIGURE 264**

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK  
QYQRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ  
REHRSMRANVELDHATLVRFS PDCRAFI VWLANGDTLRVFKMTKREDGGYTFTATPEDFFPKK  
HKAPVIDIGIANTGKFIMTASSD TTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASC  
FTPDKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV  
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH  
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQLQQQLTQ  
AQETLKSLGALKK

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

**Beta-transducin family Trp-Asp repeat protein.**

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308



TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG  
CAGTGTTTTGCCTTCACCCCAAGTGACCATGCAGAGGTTGCCACGCGAGTCTCAATCATGCTCC  
TCCTAGTAACCTGTGCTGACTGTGCTGTGATCACAGGGGCCGTGTGAGCGGGATGTCCAGTGT  
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT  
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGGCACAAGGTCCTTCTTTCAGGAACGCA  
AGCACACACCTGTCTTGTCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGCGAGGTAC  
CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGCGCCTTGCCTGGTCTCAGGATACCCA  
CCATCCTTTTCTGAGCAGACCTGGATTTTATTCTGCCATGAAACCAGCTCCCATGAC  
TCTCCAGTCCCTACACTGACTACCTGATCTCTTGTCTAGTACGCACATATGCACACAG  
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCAAGCTTGAGG  
CTGTGGTGTGAAAAGGTGGCCAGCCTGGTTCTTCTCCCTGCTCAGGCTGCCAGAGAGGTGGTA  
AATGGCAGAAAGGACATTTCCCTTCCCTCCCCAGGTGACCTGCTCTCTTCTCCCTGGGCCCTG  
CCCTCTCCCCAGATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT  
GCATTGCTCAGAGTCCCAGGTCTTGCCCTGACCTCAGGCCCTTACGTGAGGTCTGTGAGG  
ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC  
TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA  
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAAGTCAGCCTGTGGCTTGTGGCCTGTGA  
CCTGTGACCTTCTGCCAGAATTGTGATGCCTCTGAGGCCCTTCTTACCACACTTTACCACT  
TAACCACTGAAGCCCCCAATTCCACAGCTTTTCCATTAAATGCAATGGTGGTGGTTCAA  
TCTAATCTGATATTGACATATTAGAAGGCAAATTAGGAGTGTTCCTTTAAACACACTCTTTCCA  
AGGATCAGCCCTGAGAGCAGGTGTGGTGACTTTGAGGGAGGCAGTCCCTCTGTCTCAGATTGGGG  
TGGGAGCAAGGGACAGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTGAGACCAGGGAGG  
CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

**FIGURE 266**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP  
GSHKVFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

**FIGURE 267**

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGCGCAGAAGGGAGGCACTTGAGAAATGTCTTTC  
 CTCCAGGACCCAAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC  
 TGCTGCCTTGGCATTGCTGCTTGCCAAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG  
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAA  
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT  
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG  
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT  
 TTCAAAGGAGAAATCTTCCTGGATGAAAAGAAAAGTTCTATGGTCCACAAAGCGGAAGAT  
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTCTTCCGAGCCTGGAACGGAG  
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGAGTTTTTCGTGGTGGGATCA  
 GGAAAGCAGGGCATTTCTTCTTGAGACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT  
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCAAGACTTTGGCCTCAGAGAAAAAATGAT  
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATT  
 GTTTCCACTCGTGTCCTAAGGAGTGAGAAACCATTTATACTCTACTCTCAGTATGGATTA  
 TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAAATAGCCCCAAAAACAAGACTGA  
 CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA  
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG  
 TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC  
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCG  
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA  
 CACCAGTGTATTCAGCCTGGGTGACTGAGACTCTAACTAA

**FIGURE 268**

MSFLQDPSFFTGMWWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR  
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMQLDQLGVPLYAVVKEHIRTEVKDF  
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGEFILGGVFV  
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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**FIGURE 269**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCG  
 GGCCAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGAGATGCGGTAGGAGGGGCGAGCGCGAGA  
 AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCC**ATG**GCGAACCCCGGGCTGGGGCTG  
 CTTCTGGCGCTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA  
 GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG  
 GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG  
 CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG  
 CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG  
 ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATC**TAG**GTCCCCCTCTCCTGCATCTGTCTCC  
 CTCATTTGCTGTGTGACCTTGGGGAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG  
 TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG  
 GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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**FIGURE 270**

MANPGLG L L L L A L G L P F L L A R W G R A W G Q I Q T T S A N E N S T V L P S S T S S S S D G N L R P E A I T A I V  
V F S L L A A L L L A V G L A L L V R K L R E K R Q T E G T Y R P S S E E Q F S H A A E A R A P Q D S K E T V Q G C L P I

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AATATATCATCTATTATTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTT  
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTG  
GTATGTGAAGCTATTTTGGAGATCCAATTGAGGAAGCAACACATTGGAGAATGGCTACTTTCT  
ATCAAGAAATAAAGAGAACACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC  
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA  
GGGTAAATCTTGGTGTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG  
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA  
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT  
TTATTAATTTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA  
TCATATAATTTGATACAAATAAAAGAAAGTGTTCTCTCCCTTACAGAAATGACATTTTAA  
ATCGCATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAAATGACAGGGAAGAAAGGAA  
AGAAGGGAAAAATGTTGCCAGGAAAAAAA

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**FIGURE 272**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK  
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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**FIGURE 273**

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGGTTATTTCAGAGGTTTTGTTTTCTCTTAGTTCT  
 GTGCCCTGCTGCACCAGTCAAACTACTTCTTCATTAAAGCTGAATAATAATGGGCTTTGAAGATA  
 TTGTCTATTGTTATAGATCTCTAGTGTGCCAGAGATGAAAAATAATTGAACAAATAGAGGAT  
 ATGGTGACTACAGCTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA  
 GTGTATCTATATTATTTCTGTGCAATTTGAAGGAAAAATCCTCAGTACAAAGGCCAAAAACATG  
 AAAACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAAGTAGAGATGAACCA  
 TACCCACAGCAGTTTACAGAAATGTGGAGAGAAAGCGAAATACATTCACTTACCCCTGACCT  
 TCTACTTGGAAAAAAAACAAATGAATGAGCCACCAGGCAAACTGTTTGTCCATGAGTGGG  
 CTCACCTCCGGTGGGGAGTGTTTGTATGATGATCAATGAAGATCAGCCTTTCTACCGTGAAG  
 TCAAAAAAATCGAAGCAACAGGTGTTTCCGCAAGTATCTCTGGTAGAAATAGAGTTTATAA  
 GTGTCAAGGAGGGAGCTGTCTTAGTAGAGCATGCAGAAATGATTTCAACAAAACTGTATG  
 GAAAAGATTGTCAATTTCTTCTGATAAGTACAAACAGAAAAAGCATCCATAATGTTTATG  
 CAAAGATTGATCTGTTTGAATTTTGTAAAGCAAAAAACCCATAATCAAGAAGCTCCAAG  
 CCTACAAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATT  
 TTAAAAACACCATACCATGGTGCACCACTCTCCACCTGTCTTCTATTGCTGAAGATC  
 AGTCAAAAGATTGTGCTTGTAGTCTTGATAAGCTTGAAGCATGGGGGGTAAAGACCGCT  
 AAATCGAATTGAATCAAGCAGCAAAACATTTCTGCTGCAGACTGTTGAAATGGATCCTGGG  
 TGGGGATGTTCACTTTGATAGTACTGCCACTATTGTAATAAGCTATTCCAAATAAAAAGC  
 AGTGATGAAGAAGACACATCATGCGAGGATTACCTACATATCCTCTGGGAGAACTTCCAT  
 CTGCTCTGAATTAATAATGCTATTTCAAGTGATTTGGAGAGGTACATTTCCCACTCGATGGAT  
 CCGAAGTACTGTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTGATTTGATGAAGTG  
 AAACAAGAGTGGGGCATTTGTTGATTTTATGCTTTGGGAAGAGTGCTGATGAAGCAGTAT  
 AGAGATGAGCAAGATACAGGAGGAAGTCAATTTTATGTTTCAGATGAAGCTCAGAACATG  
 GCTCATTTGATGCTTTGGGCTCTTACATCAGGAATATCTGATCTCTCCAGAGATCTCCCTT  
 TGATCTGAAATGAAGGATTAACACTGAATAGTAATGCTTGATGAACGACACTGTCTAAT  
 TGATAGTACAGTGGGAAGGACACGTTCTTTCTCATCACATGGAACAGCTGCTGCCACAGTA  
 TTTCTCTCTGGGATCCAGTGGAAACAAATAATGAAAAATTTACAGTGGATGCAACTTCCAAA  
 ATGGCCTATCTAGTATTCAGGAAGTGCAAAGTGGGCATTTGGGCATCAATCTTCAAGC  
 CAAAGCGAACCCCAAGACATTAACATTACAGTAACCTCTCGAGGACGAAATTTCTTCTGTGC  
 CTCCATACAGTGAATGCTAAAATGAATAAGGACGTAACAGTTTCCCAGGCCAATGATT  
 GTTTACGCAGAAATTTACAGGATATGTACCTGTTTCTGGAGCCAATGTGACTGCTTTTAT  
 TGAATCACAGAAATGGACATACAGAAGTTTGGAACTTTTGGATAATGTTGACGGCGCTGATT  
 CTTTCAAGATGATGGAGTCTACTCCAGGTATTTACAGCATATACAGAAAAATGGCAGATAT  
 AGCTTAAAAGTTCCGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTACGGCTCCCAT  
 GAATAGAGCCGCTGATACATACAGGCTGGGTAGTGAACGGGAAATTTGAAGCAAAACCCGCCAA  
 GACCTGAAATTTGATGAGGATCTCAGACCCTTGGAGGATTTACGCCAAGCAGCATCCCGGA  
 GTGTGCATTTTGGTATACAAAGTCCCAAGCCTTCCCTTGCCCTGACCAATACCCCAAGTCA  
 AATCACAGACCTTGATGCCACAGTTCATGAGGATAAGATTATCTTACATGGACAGCACCAG  
 GAGATAATTTTGTGTTGGAAAGTTCAACGTTATATCATAGAATAAGTGCAAGTATCTCT  
 GTCTTAAGACAGCTTTTGTATGCTCTTCAAGTAAATACTACTGATCTGTCAACAAAGGA  
 GGCAACTCCAAAGAAAGCTTGCATTTAAACAGAAATATCTCAGAGAAATGCAACCC  
 ACATATTTATTTGCCATTAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATT  
 GCACAAGTAACTTTGTGTTATCTCCCTCAAGCAAACTCTGATGACATTGCTACACCTATCC  
 TACTCTCATCTCTCTCTGATAAAAGTCAATAATCTGGAGTTTAAATATTCTACGCTGGTAT  
 TGTCTGTGATTTGGTCTGTTGTAATTTGTTAACTTTATTTAAGTACCACATT**TGA**ACTTAA  
 ACGAAGAAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTTAAAAACAAAAATGTAAGT  
 AAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAACTCATAAAAATAATT  
 TTAGATGTCCGAAAGGATACCTTTGATTAATAAAACACCTCGGATATGTAAGAACTGT  
 CAAGATTAATAATTAAGTTTCACTTTATTTTATTTTGAAGAAATAGTGATGAAC  
 AAAGATCCTTTTCTACTGTACCTGGTGTATATTTATTTGATGCAACAGTTTCTTGAAT  
 GATATTTCAAAATGTCATCAAGAAATTAATAATCATCTATCTGAGTAGTCAAAATACAAGTAA  
 GGAGAGCAATAAACAACATTTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 274**

MGLFRGFVFLVLLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY  
 LFEATEKRFFFKNVSIILPENWKENPQYKRPKHENHKHADVI VAPPTLPGRDEPYTKQFTEC  
 GEKGEYIHFPTDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR  
 CSAGISGRNRVYKQGGSCLSRACRIDSTTKLYGKDCQFFDPKVQTEKASIMFMQSIDSVVE  
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLV  
 LDKSGSMGGKDRLLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM  
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGDNNTASSCIDEVKQSGAIVH  
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNGLIDAFGALTSGNTDLSQKSLQLESKGLT  
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG  
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG  
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDDGVYSRYFTAYTENGRYSCLKVRAHG  
 GANTARLKLRLPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLLEDFSRTASGGAFVVSQV  
 PSLPLPDQYPPSQITDLDTVHEDKIIILTWTAPGDNFDVGKVQRYIIRISASILDLRDSFDD  
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP  
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

**FIGURE 275**

CTCTTAGGTGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCTCCG  
 GGCAGGGGTGACAAACAGGTGTCATCTTTTGTACTCGTGTGTGGCTGCCTCTCTATTCAAAGGAAAG  
 ACGCCAGGATTAATTTGCCAGAGGAGCAATGATGTAGCCACCTCTCAACCTTCCCTTCTTTGAACC  
 CCCAGTTATGCCAGGATTTACTAGAGAGTGTCACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTT  
 TGGTCTGGAGGAGAGAACCTTTTGGGGCTGCGTTTCTCTTAGCAGTGTCTCAGAAAGTACTTGGCTGA  
 GGGTGGAGCCAGAGAAAGGAAAGGTCCCCCTCTGTGCTTGGCTGCAATCAGGAAGGCTGTGATGGG  
 ATGAAGGTGAAACTTTGGAGATTTCACTTCAGTCACTTGCCTGCCTCAGAGTCACTCTTTAAAA  
 GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAGGAAAGATGGATG  
 CAAGCAGCTCCGGGGGCCCAAAACGCATGCTTCTGTGGTCTAGCCACGGGAAGCCCTTCCCTGGG  
 GCCCCGGCTTTGAGGGATGCCACCGGTTCTGGAGCGCATGGCTGATTCTGAAATGATGGTTGGCC  
 GGGGGCTGCTTGGCTGGATTTCCCGGGTGGTGGTTTGGCTGGTGGCTCTGCTGTGCTATCTCTCT  
 CCTGTACATCTTGGCCCTGCACCCCAAGGTGACGAGGAGAGCTGGCACTGCCAGGCCAACAGC  
 CCCACGGGAAGAGGGGTACACGCGCTCTTCAGGAGTGGAGGAGCAGCCCACTACGTGAA  
 GCAGCCTGAAGGCGCAGATGCCACAGCTCAAGAGGAGCTGAGGAGGAGTGAAGCAGCTCAGGAA  
 TGGCAGTACCAAGCCAGGATGCTGTGGCTGGTCTGGACAGGAGCCCCCAGAGAAACCCAG  
 GCCAGCTCTCGGCTTCTGCTCACTGCGAGGTGGACAAGGCAGAGTGAATGCTGGCGTCAAGCTGG  
 CCACAGAGTATGACAGAGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACACGCTGGAGACTGG  
 CCTTACC CGCCACCCCGAGGAGAACCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCCATT  
 GAATCAGCCTTTGGAGACCCCTGAAACAATCCTGCAGAGAACAGCCCCAATCACCGTCTTACACGGCT  
 CTGATTTTCATGAAGGAGTCTACCGAACAGAAAGGGACATTTGATGAGCTCACTTCAA  
 AGGGGACCAACAAACGAATTCAAACGGCTCACTTAACTTCGACCATTCAGCCCAATCATGAAGGT  
 AAAAATGAAAAGTCAACATGGCCCAACAGCTTATCAATGTTATCGTGGCTCTAGCAAGAAAGGGTG  
 ACAAGTTCGGCGAGTTCATGCAAGATTTGAGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCT  
 CACTGTTGTTTACTTTGGGAAGAGAAATAAATGAAGTCAAGAGAACTGCAATCAACATCTCCAA  
 GCTGCCAATCTCAGGAATTTTACTCTTACCTCAGCTGATGGAGAAATTTCTCGGGGAAGAGGAGTGA  
 ATGTTGAGGCCCGCTCTGGAAGGGAAGCAGCTGCTTCTCTTTCTGTGATGTGACATCTACTTT  
 CACATCTCAATTTCTCAATAGCTGTAGCTGAATACACAGCCAGGGAAGAGGTATTTATCCAGTT  
 CTTTCTGCTCAGTCAATCTCGCATTAATATACGGCCACCATGATGCAGTCCCTCGCTTGGAAACAG  
 AGCTGGCTATAAGAGAGAACTGGATTTGGAGAGACTTTGGATTTGGATGAGCTGTCAGTATCG  
 GTCAGACTTCATCAATATAGTGGTGGTTTGTACTGGACATCAAAGGCTGGGGCGGAGGAGTGTGCAC  
 CTTTATCGCAAGTATCTCCACGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTTTCGCC  
 TCTGGCATGAGAAGCGCTGCATGAGCAGCTGACCCCGAGCAGTACAAGATGTGCATGCACTCCAA  
 GGCCATGAACAGGAGCATCCACCGGCCAGCTGGGCATGCTGGTGTTCAGGCACGAGATAGAGGCTCAC  
 CTTCCGAACAGAAACAGAGACAGTAGCAAAAAAATGAACTCCACAGAGAAGGATTTGGGGAGA  
 CACTTTTCTTTTCTTTTGCATTAAGTGGCTGCAACAGAGAAAGACTTCATTAAGGAGCG  
 ACAAAAGAAATTTGACTGATGGGTGAGAGATGAGAAAGCCCTCCGATTTCTCTCTTGGGCTTTTAC  
 AACAGAAATCAAAATCTCCCGTTTGGCTGCAAAAGTAAAGCAAGTGTCACTCTGTGAAGTGTGACA  
 AAGGCAGAACTGTTGTGAGATTTAAGCTTAATGGTGTGGAGTTTGTATGGTGTTTTACAATACAT  
 GAGACCTGCTGTTTGTGCTCATTTGAATGATTTGATGATTTAAGAGCAGTTTGTAAATTAATCTAT  
 TAGCATGAAGGCAAGCATATTTCTCCTCATTAATGAATGAGCCATCAGCGGCTGATGTTTCTAGG  
 AATGCTAAATATCAGAAGGCGAGGAGGAGATAGGCTTATTATGATCACTAGTGTGAGCATTAAGTA  
 AATAAATGGACCAGAAAGAAAGAAACCATAAATCTCGTGTATATTTCCCAAGATTAACCA  
 AAAATTAATCTGCTATCTTTTGGTGTCTTTTAACTGTCTCCGTTTCTTTTCTTTTATTTAAAAAT  
 GCACTTTCTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTAACCATTTGCAAGCTTTACAAGAGA  
 GCACAGTGTGGCTTACATTTTATTTTAAAGAAATGATTTGATAGTATTTGAGAACTTTCA  
 GTTCAAAAGCATCAAAATGATGCCATATCCAAAGGACATGCCAAATGCTGATTTCTGAGGCATTAAT  
 GTCAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGAGCTACAGATCTTCTGGA  
 GAGTATTTTCAAGAGGAGCAACTGAACACTGGAGGAAAGAAATGACATCTTCTGCTTCTGGA  
 AAGGAACTCATTCAGCTGCTGTATCTGATCTTAACTTAACTTCAAGAACTCATCTTCTGGA  
 GAAGTAGGACCGCTTCTTACCTGTTTAAATAAACCAAGATACCGTGTGAACCAAACTATCTCT  
 TTTCAAACAGGGTGCCTCTGGCTTCTGGCTTCCATAGAAGAAATGGAGAAATAATATATAT  
 ATATATATATATTTGGAAGATCAATCCATGCGCAAACTAGTGGGATGGAAGTTTGTGCTACAT  
 GTTATCCACCCAGCGAGGTAAGTAACTGAAATTTTAAATTAAGCATTTCTACTCAATCA  
 CCAAGATGCTTCTGAAATTTGCATTTTATTACCATTTCAAATCTTTTAAAAATTAATACAGTTA  
 ACATAGATGGTTTCTTCACTATGTGAAATATTAAGGCAGCAGCAGATGGCATGAGCTAATTTATCT  
 CTTTGGTCCCTTGTCTTGTGTTGCTCAGATAAATCATTTGTTTAAAGCTTCAAGAACTCAAGC  
 GTTGGTGTGTTAAAAAATGATTGATTGATTTGATGTTGATGTTTAAATTTAATTAACCAAC  
 AGGCCATGAATGGAAGGTGGTATTGACACGCTAATAAATATGATTTTGGATATGAA

**FIGURE 276**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ  
EWEEQHRNYVSSLRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL  
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDELVEAIES  
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP  
MKVKNEKLNMAINTLINVIPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK  
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR  
LNTQPGKKVFYPVLFSEQYNPGIIYGHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI  
NIGGFDLDIKGWGGEDVHLYRKYLSNLIVVRTFVRGLFHLWHEKRCMDELTPEQYKMCMQS  
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

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**FIGURE 277**

GAAAGAATGTTGTGGCTGCTCTTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAACC  
 AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT  
 ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA  
 GTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT  
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC  
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACT  
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG  
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT  
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT  
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG  
 GGGCATATTAATGATGCCTTCTGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT  
 TGTTCTGCTTCTCAAGAAATTAACATTGTGTTCTGTGTGACTGCTGAGCATCCTGAAATA  
 CCAAGAGCAGATCATATATTTTGTTCACCATCTCTTTTGTAAATAAATTTTGAATGTGCT  
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAGCTATTACAGAC  
 TCAAAATATTCTAAAATATTTTCTGACAGTATAGTGATAAATGTGGTCATGTGGTATTTG  
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC  
 AAAGACCTAAGGAAAAATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT  
 TGAAGTGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG  
 TGAGAAGTAATTATTGTAAATGGATGGATAAAATGGAATTACTCATATACAGGGTGGAATT  
 TTATCCTGTTATCACCAACAGTTGATTATATATTTCTGAATATCAGCCCCTAATAGGAC  
 AATTCTATTGTGGACATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG  
 TAATAATCATCTCTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 278**

MLWLLFFLVTAIHAE LCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP  
NREATEISHVLLCNVTQRVSFVVTDP SKNHTLP AVEVQSAIRMKNRINNAFFLNDQTLE  
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIAL LLSGIWQRRRKNKEPSEVDDAEDKC  
ENMITIENGIPSDPLDMKGGILMMP S

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**FIGURE 279**

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG  
 GTGTTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGT  
 ATGGCAAGAGCTCTACTCGTGCCTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG  
 CCTATAGCAGCTGTGGAAATTATACCTCCCGGGTGTGGAGGCTGTTAATGGGACAGATGC  
 TCGGTTAAAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA  
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC  
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA  
 TGCCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATAACCTGCCAGGTGA  
 AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA  
 CGCTTCTCTGAGATCCACTTCTTGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT  
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC  
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT  
 GTTTATTTAGAAGACACAGACTAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA  
 GAACCCTAGTATTTCTTGAAGTTAATGGAAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT  
 TTTCCAACAGTTCTGCGAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC  
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA  
 GTGTAATATTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTGGCCTTAA  
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAGGGGATAAAAGCC  
 AATTTGTCTGTTACATTTTCCTTTACGTATTTCTTTAGCAGCACTTCTGCTACTAAAGTTA  
 ATGTGTTTACTCTCTTCTCTCCACATTCTCAATTTAAAGGTGAGCTAAGCCTCCTCGGTG  
 TTTCTGATTAAACAGTAAATCCTAAATTCAAACTGTTAAATGACATTTTATTTTATGTCTC  
 TCCTTAACTATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT  
 TTTGTCG

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**FIGURE 280**

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT  
WNFRPLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ  
VKNPPDVGVIQEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAER  
AHKVVEIKSKEERLNQEKVSVYLEDTD

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**FIGURE 281**

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT  
ACTCTTGGGAGTTTCCATCTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG  
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT  
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG  
TAAAGACATTCCAGTTTACCCAAATGGGTGGGGATCTCCGAATGGTAGAGTGTGTCCCT  
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTCATGCTTCCTGTGATTTC  
ATCCAACACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA  
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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**FIGURE 282**

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGFPADDEAPDAETTAATTATTAAPTTAT  
TAASTTARKDIPVLPKWVGDLNGRVCP

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GGACTCTGTAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC  
CTAGGGGTCTGGATTGCTGGTTAAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC  
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA  
GTGTCTGGGTCAAGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC  
ACTTGGCAAGGTCACGCATGCTCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG  
GACAGTTCGTGTTGTGCTTGGTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG  
GCAAACTCCATAAAGAACAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT  
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAAAACCACAGGCTG  
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA  
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAGGAGGAGGAGG  
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCAGCTTTGGGAGGCCAGGCGGGTGGAT  
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA  
TACAAAAAATTAGCCAGGCACAGCTGGTGTGCGAGTGAGTCTTACTCGGAGGCGCTGAG  
CGAGGAAAATCGCTTAAGACCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT  
TCCAGCCTGGGGCGACAAGAGTGAGACTCCATCTCACACA

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**FIGURE 284**

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG  
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

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GTCA**TCAG**CCAGTGCCTGCTCTGTGCTGCTCTGGGCCCTGGCAATGGTGACCCGGCTGCCTCA  
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG  
GACCTGCACTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA  
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC  
CGGGGCCGGGATGCAGCCAGGAACCTTGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA  
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCCAGAA  
AGGTGCTACGGGACAGCGTGCAGCGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT  
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCTATGGGC  
CCTCAGAGCCACGTGCAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC  
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCCT**TCGA**ATCTGCCTGGATGGAAC TGAG  
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGGAGGAGCTG  
CCTGTTCACTGGGATCAGCCAGGGCGCGGGGCCCACTTCTGAGCACAGCAGAGACAGCAG  
CGAGCGGGGACAAAGGACAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA  
CCCTTTCATGCCTACACACCCCTCATTAAGCAGAGTCTGGCATTTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 286**

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRGTK  
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK  
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ  
IQLRLHTAALPA

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**FIGURE 287**

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAAATTGTCAT  
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA  
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC  
 TGGACAGAAGTCAATGCCTTGAAGGAAATCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC  
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG  
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCCGACGAAATCAACGCC  
 CTCCAAGACTATGGTAAAGGAGCCTGCCAGGTGTCAATGACTTTTGCTGGGCATCAATGA  
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG  
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAAGTGTGCTCTCTCCCAATCAGCTCAG  
 GGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATACATATGCGAGTTCACCATCCC  
 TAAAT**TAG**GTCTTTCTCCAATGTGTCTCCAAGCAAGATTTCATCATAACTTATAGGTTTCATGA  
 TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAAAAAATTGCAACACAAGATCAAT  
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT  
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT  
 AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA  
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT  
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT  
 GCTATATAATCCAAAACTTTTCAGCCTGTGTCTCATTCTGTCCCATGTCTGGCAATAATACC  
 TTGTACAGCCATTACCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT  
 GCCATATCAGAACACAAACCCCTGAAGAGTTTCTGATTTGATTTTTTTTTTTTCTTCATGCC  
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGTAT  
 CAATTTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT  
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT  
 AGCATCCTTACTCTACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT  
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT  
 TGGAGCTGAAAACGAATTTAAAGAATGCTATCTTGAAAAATTGCATACGCTGTGTGAATT  
 TTTTATTTCTGCCTAGTGCATTCTGCTTGTTTAACTAGATTGTACAAAATAAATTCATTGCT  
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAATGGGCTTTTTAGAAAGCAAAATTTT  
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT  
 CCCACTTTGCAAACCTTAACTACACATGCTTGGAATTAAGTTTTAGCTGTTTTTCATTGCTCA  
 ATAATAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 288**

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT  
EVNALKEIQALQTVCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ  
DYGKRS LPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSQAQCK  
WSDEACRSSKRYICEFTIPK

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GCAGGAGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGAGGTTCCCCGCGCG  
CCCGAGCCCCCGCGCCATGAAGCTCGCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTGCA  
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCACGCTGTGCTGCGCTG  
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCTTGGCCAACCCCTCGGCACCTCAACCCGCT  
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCAGAAGT  
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG  
GCCCTGACAGTGTTTGCTTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC  
CACC CGC GAGGGCTGAAAAACCCCGCGCGGGGAGGACCGTCCATCCCTTCCCCGGCCCT  
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 290**

MKLAALLGLCVALSCSSAAAFIVGSAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLLLS  
SLGIPVNHLEGSQKCVaelGpQAVGAVKALKALLGALTVEG

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**FIGURE 291**

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT  
 CCTTGGCCTCCGCGAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTG  
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCC  
 TCAGAACCCAGACCAGCAGGTAGTGCAGGCTCCAGGGAGGAAGAGGAGATGAGCAGGAGG  
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAACCTGGCTGATGGCCAGCAGGCAGCAGCTT  
 GCCAAGGAGACTTCAAACTTCGGATTACGCTGCTGCGAAAGATCTCCATGAGGCCAGATGG  
 CAACATGGTCTTCTCTCCATTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCA  
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG  
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCGCCAACCTGGAAC  
 GGGCCTCTCACAGGGGAGTTTGCCTTATCCACAAGGATTTTGATGTCAAAGAGACTTTCT  
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCTATGAATTTTCGCAATGCCTCA  
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAAGAGACTCGGGGGAAAATTTCCAAACT  
 GTTTGATGAGATTAATCCTGAAACCAAAATTAATCTTGTGGATTACATCTTGTTCAAAGGGA  
 AATGGTTGACCCCATTTGACCTGTCTTACCAGAGTCGACACTTTCACCTGGACAGTAC  
 AAGACCATTAAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA  
 TTTTCGTTGTGCATGCTCCTCAAACTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA  
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA  
 TGGCTCAGAACATGAAAACCCAGAAAACATGGAAGTTTCTTTCCGAAGTTCAGCTAGATCA  
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTACCCCTTTG  
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTACGAAGA  
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATAC  
 TGCTTATTCATGCTCTCTGTCATCAAAGTGGACCGGCCATTTTCATTCATGATCTATGAAG  
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGTGGTGAATCCGACTCTCCTATTAATTCAGG  
 ACATGCATAAGCACTTCTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA  
 TACCAGCAATGGATGGCAGGGGAGAGTGTCTTTTGTCTTAACTAGTTTAGGGTGTCTC  
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCGAGCAGATGC  
 CTGAAACGGTGGACAGTGTCTGAACCTTATATATATTTTCTTACATACATACCTATGAT  
 AAAGTTTAAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAAACAACATTAAGTAAAA  
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA  
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAAATCA  
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCATCCACTACTCAGAATGGCATGC  
 TGCTTAAAGACTTTTAGATTGTTTATTTCTGGAATTTTTCATTTAATGTTTTGGACCATGGT  
 TGACCATGGTTAACTGAGCTGCAGAAAGCAAAACCATGGATGGAAGGAGGACTACTACAAAA  
 GCATTAATGTATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

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MKVVP SLLS VLLA QVWL VPGL APSQSPET PAPQN QTSRVVQAPREEEDEQEASEEKAGE  
 EEKAWLMASRQQLAKETS NFGFSLLRKISMRHDGNMVFSPFGMSLAMTGLMLGATGPTETQI  
 KRGLHLQALKPTKPGLLPSLFKGLRETL SRNLEGLSQGSFAFIHKDFDVKETFFNL SKRYF  
 DTECVPMNFRNASQAKRLMNHYINKETRGI PKLFEINPETKLILVDYILFKGKWLTPFDP  
 VFTEVDTFHLDKTKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHL  
 ALEDYLTDLVETWLRNMKTRNMEVFFPKFKLDQKYEHELLRQMGIRRIFFPFDLSLSA  
 TGRNLQVSRVLRRTVIEVDERGTEAVAGILSEITAYSMPVVIKVD RPFHMIYEETSGMLLF  
 LGRVNP TLL

**FIGURE 293**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAG  
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG  
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG  
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTTCCC  
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCA  
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCTGGGCCGTGTCTGAGTCCC  
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC  
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGAGGAAGACCAAGACCACA  
TCTACCACCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAGGCCAGG  
CTGTTGGGACTGGGACCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA  
AAAAAAAAAAAAAAAA

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**FIGURE 294**

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL  
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE  
RPRLWVMPNHQVLLGPPEEDQDHIYHPQ

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**FIGURE 295**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGAGTGAAGGAGCTCTCTG  
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC  
 TGTTCCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA  
 TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC  
 TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT  
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATG  
 CGTGGGAAGTGACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC  
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG  
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCAGTG  
 CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC  
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT  
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC  
 GACGCCCAGAAAACAGCATCTTATTACTACCCCTATGGCCAGCGGGAATTCAGTGCGGGATT  
 GTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG  
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCAGAGGCCAGT  
 CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACCTCATGTTGGTTA  
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTGTG  
 GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA  
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

**FIGURE 296**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN  
GVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGDRWSSQGGSKADYPEGDGNWANYNTFG  
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI  
YQKYPVKYGEGKCWTDNGPVI PVVYDFGDAQKTASYYSYPYGQREFTAGFVQFRVFNNERAAN  
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL  
FYR

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**FIGURE 297**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC  
 CACGAGGCTGCCGCATCTTGCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG  
 CGCTGCTCTCTGGGACGCTGCAGGTGCTAGCGTGCTGGGGGCCGCCATGAAAGCGCAGCC  
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGTAACCTCAAC  
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC  
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG  
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC  
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG  
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT  
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACGGGAGCTTTGTTGGTGGTATTGTATTAAC  
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTTC  
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA  
 ATACAGATTGATGCTGCCTATCAATTAATTTTGTTTATTAATAGTTTAAAAACAATATTCT  
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGATTACGTAAATATGTA  
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT  
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCTATCTTTTTTTTTTGGCT  
 GGGGTGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA  
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT  
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA  
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTAAAGAAAACATCAACATTTTTTG  
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

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**FIGURE 298**

MGLGARGAWAALLLGTLLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPSDH  
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN  
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG  
CKMYYSRRGIRYRTIDEHDAII

0999725.11204

**FIGURE 299**

CAGCCGGGTCCTCCAAAGCCTGTGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG  
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGCGCAGCCCTGTGGGAGGC  
 CTTCTTCGGCTTGGCTCCTTGTCTAGCCTGTCTGTGCCTGGCGCTTCCGTGCTGCTGCTGGC  
 GCAGCTGTCTAGACGCCGCAAGAAATTCGAGGATGTCTAGATGTAAATGTATCTGCCCTCCCT  
 ATAAAGAAAATTCCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCCTT  
 CATGTTGTGGAGCCCATGCCCTGTGCGGGGCTGATGTAGAAGCATACTGTCTACGCTGTGA  
 ATGCAAATATGAAGAAAGAGCTCTGTCAACAATCAAGGTTACCATTATAATTTATCTCTCCA  
 TTTTGGGCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG  
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT  
 TGCAAATGCACAGCATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG  
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG  
 CATGTTGTCTCTCAGCTAAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA  
 CTGGAAGAAGTCTGACTGGGTTTTGCTGGGTTTCAATTTAATACCTTGTGATTTCACCAACT  
 GTTGCTGGAAGATTCAAAGTGAAGCAAAAGTCTGCTGATTTTTTTTCTTGTGTTAACGTA  
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTTATTG  
 TGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCTTTTACCTGGAACA  
 AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAAGGTTTTTG  
 TTGTTGTTGTTTTTGTGTTGTTTGTGTTGGGAGAGGGGAGGGATGCCCTGGGAAGTGGTT  
 AACAACTTTTTCAAGTCACTTTACTAAACAACTTTTGTAAATAGACCTTACCTTCTATTT  
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG  
 ACTTTTGCAGTACTGTATTATCTGGGTATCTGCTGTGCTGCATTCATGGTAAACGGGAT  
 CTAAATGCCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG  
 CAATGCATCCTAGAACAAGTGGCCATTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG  
 GTGTGTGTTGCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT  
 TGCAATAAAGAAATTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG  
 TCAGCATTTCCGGTCGTGGTGAGAGGCAAGTGTGTTGAGCTCCAATATGTGCAGCTTTGAAC  
 AGGGCTGGGGTGTGGGTGCTCTTCTGAAAGGTCTAACCATTATTGGATAAAGTGGCTTTTT  
 TCTTCTATGTCCTCTTTGGAATGTAACAATAAAAAATAATTTTGAACATCA

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**FIGURE 300**

MATLWGGLRLGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS<sub>GH</sub>IYNKNIS  
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTII<sub>II</sub>YLSILGLLLLY<sub>MY</sub>LTL  
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ  
RKSVFDRHVLS

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T002T-324860

**FIGURE 301**

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT  
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCC GCGGAAGCGG  
CAGGAGCCGCGCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA  
CCAGGCACCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG  
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG  
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT  
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATGA<sup>1</sup>AAATCTAATATGGCGATAAAAA  
TCATTGTCTACATTAA<sup>2</sup>AACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA  
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCA<sup>3</sup>GTTCACATAA<sup>4</sup>GAATG  
TTTACTCAATGTTTAAGTGT<sup>5</sup>TTTGCCCCAA<sup>6</sup>AATTCACA<sup>7</sup>ACTACAAGGCAGA<sup>8</sup>ACTAGGACTT  
GAACATGGATCTTTTG<sup>9</sup>GTCTTAATCCAGT<sup>10</sup>GAGTGATACAATTCAATGCAC<sup>11</sup>TCCCCTGCCA

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302/330

**FIGURE 302**

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRFPPMMHHHQAPSDGQT  
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPIYGFIFLYILYILFKVSRILI  
ILHQ

09989725-112001

**FIGURE 303**

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAAGTGCATTGCCTCCCTGGGTGCTCTTCATCTT  
GGATTGAAAGTTGAGAGCAGC**ATG**TTTTGCCCACTGAAACTCATCTGCTGCCAGTGTTAC  
TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTTCCCGCCTGAGCTAACAGTCCATGTG  
GGTGATTACGCTCTGATGGGATGTGTTTTCCAGAGCAGAGAAGACAAATGTATATTCAAGAT  
AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA  
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGACATCTTATGC  
AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA  
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG  
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGATGTGTTTTCCAG  
AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA  
GGAGATTGTATTTGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG  
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTCCGCAATGACGGTCCATCATG  
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT  
GGTGTTCAGAAAACCATTTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCC  
CGGCAGCCCTGAGGCCCTTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC  
TGTGCCACAATCTGTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA  
GAGTTCAGTGAATCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG  
AAAAACCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA  
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGA AAAATCAGAGGCCACCTACATGACCATGCA  
CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG  
GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG  
TGGAGACTCTCTCTGTGTGTGCTCGGGCCACTCTACCAGTGATTTCAGACTCCCCTCTC  
CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG  
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC  
CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT  
GGATCAGACCTCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA  
AAACCAACCAATCAA

MFCPLKLILLPVLLDYSGLNLDNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLSPG  
EHAKDEYVLYYYNLSVPIGRFQNRVHLMGDILCNDGSSLLQDVQEAQGTYYICEIRLKGES  
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY  
HKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSI MLQGVRES DGGNYTCSIHLGNLVFKKTI V  
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLPVLLIVKKTCGNKSSVNSTV  
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWP SLR  
SDRNSNLEKSGGGMPKTKQAAF



**FIGURE 305**

CTATGAAGAAGCTTCCTGGAACAAATAAGCAAAGGAAACAAATGTGTCCCATCTCACATG  
GTTCTACCCCTACTAAAGACAGGAAGATCATAAAGTACAGATACTGAAATTGTAAGAGTTGG  
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA  
GGATGAAGATGGATACATCACCTTAAATATTAAGAACTCGGAAACCAGCTCTCGTCTCCGTTG  
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG  
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTGGTCTGTGATGCAGCGCAATTACCTACAAGA  
TGAGAATGAAAATCGCACAGGAAGTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG  
TAAACAATCAGAACTAAAGGGCACTTCAAAGGTCATAAATGCAGCCCTGTGACACAAAC  
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG  
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG  
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT  
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA  
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCCTACCTTCTGTG  
AGAACAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT  
**TAA**TGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAGATATGT  
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

**FIGURE 306**

MQDEGYITLNIKTRKPALVSVGPASSSWVRMALILLILCVGMVVGLVALGIWSVMQRNYL  
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE  
ESKQYCTDMNATLLKIDNRNIVEYIKARHLIRWVGLSRQKSNEVVKWEDGSVISNMFEFL  
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

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CCACACGCTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCGCATCCGG  
CCCCGGGGTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCAG  
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCTTTGCTGAAGCCCGAGTCGGAGAA  
GCCCCGGGCAAACGCGAGGCTAAGGAGACCAAAGCGCGGAAGTCGCAGACAGCGGACAAGCAG  
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAGAAGCGGTGGTGGTGGG  
CGTCGTGGCCATGCGCGGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG  
AGCGCGAGAAATCCAACGCTGCAAGTGTGTGACGAGCCCCAGCAAAGGCAAGACCAGCTGC  
GACAAAAACAAGTTAAATGTCTTTTCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG  
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC  
ACTTCGAGCTGCAAGGCGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT  
CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT  
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTACACCTGAGTGCA  
AATTCAAAGAATCAGTGTTTGAATAATTATATGTGACATATTCATCAATGATATACCGTCAG  
CAGCAGTCAGGCCGAGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAGGCAA  
CCATGTGAAGAAGAACAGCCTGCAGCTCATTTTCTGCCTAAACCATTGAAAGTGCCCATGT  
ACAAGGAGCCATCACTGCACGATCTCACGAGTGTCTCCGATCTGGAAGCGGGACCCCAAC  
AAGACGAGAAGTGCTCTGGCGTGCTGACGAGGAGCAATCCATGAGCCACAATGAATCAAC  
**TAG**CCAGTGTAGGGCAAAGAGGGCTCTGCTAACAGAACCTTACCTCCAGGTGCTGTTGAAT  
TCTTCTAGCAGTCCTTACCCCAAAGTTCAAATTTGTGAGTGACATTTACCAACAAACAGG  
CAGAGTTCCTATTTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

**FIGURE 308**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498  
><subunit 1 of 1, 245 aa, 1 stop  
><MW: 27564, pI: 10.18, NX(S/T): 1  
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNKLNVFSRVKLFSGSKRRRRRP  
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA  
MNSEGILYTSSELTPECKFKESVFENYYVTYSSMIYRQQSQSGRWYLGLENKEGEIMKGNHVK  
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

**N-glycosylation site.**

amino acids 242-246

**Glycosaminoglycan attachment site.**

amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site.**

amino acids 93-100

**N-myristoylation site.**

amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop).**

amino acids 231-239

**HBGF/FGF family proteins**

amino acids 78-94, 102-153

**FIGURE 309**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG  
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG  
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCC  
 CCATTTAGAGTGTAGCAAAGGAAAAAACCAAGGTTGGGTTCTTCTCTGACATTGGCAGTG  
 CCCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCCACACCTGTAGATTAC  
 AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA  
 ACCACGTCTTGGAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACTG  
 GAGAGGAGGGAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG  
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACTGGCTGCT  
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGGCAG  
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGTCTCTCTGGGGGAGCCAG  
 CGCGCTCCGGGCCTGCCGTTTGGGGGTGTCTCCTCCGGGGCGCTATGGCGCGCTGGC  
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGCGAGCCGGCCGGTGTGCG  
 CGCAGCGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCTG  
 CTGTCCAAGTGCGACTGTGCGGGGGCGGCCCGCGCGGCCGAGCCGCGGCCCGGAGCCTCA  
 GCTCAAAGGCATCGTCACCAAAGTGTCTGCGCCAGGGTTTCTACCTCCAGGCGAATCCCG  
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGTCTCTTACCCACTTCAACCTGATCCCT  
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC  
 TGAGGGACTGCTCTACAGTTGCGCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT  
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTTACCGCCAGCGTCGTTCTGGCCGGGCC  
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTGATGAAGGAAACCGAGTTAAGAAGACCA  
 GGCAGCTGCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC  
 ACAGTGTCCCGAGGCCTCCCTTCCAGTCCCCTGCCCTTGAAATGTAGTCCCTGGACTG  
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

**FIGURE 310**

MAALASSLIHQKREVREPGGSRPVSQAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR  
GPEPQLKGIVTKLFCRQGIFYLQANPDGSIQGTPEDTSSFTHFNLI PVGLRVVTIQSAKLGHY  
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR  
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

**Tyrosine kinase phosphorylation site:**

amino acids 199-207

**N-myristoylation sites:**

amino acids 54-60, 89-95, 131-137

**HBGF/FGF family signature:**

amino acids 131-155

**FIGURE 311**

**ATG**GCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG  
GGACCGGCCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGGCTCTGCAACG  
GCAACCTGGTGGATATCTTCTCCAAAGTGC GCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG  
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT  
GCAAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT  
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGAGTGAAAACAGGGTTGTAT  
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT  
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG  
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA  
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG  
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA  
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAGAGTAAGACAACA**TAG**

CGCGGCCGCTCTGCAACG

**FIGURE 312**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
```

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKQAREQHWDRPSASRRSSPSKNGRLCNGNLVDIFSKVRI FGLKKRRLR  
RQDPQLKGI VTRLYCRQGYILQMHPDGDALDGT KDDSTNSTLNLIPVGLRVVAIQGVKTGLY  
IAMNGEGYL PSELTFTPECKFKESVFENYVIYSSMLYRQGESGRAWFLGLNKEGQAMKGNR  
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site.**

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198



GGGGAGGGAATTGAACATTGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTCCTTGCACAAAAT  
GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACCGAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA  
ACGAAGCTTTTTCTTTGTGAGCCCTGGATCTTAAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAAT  
AAATAAACCCAGGCTTAGACCCCGGGGGTGGTGGTGTCTGACATAAATAAATCTTTAAAGCAGTGTCTCC  
CTCCCACCCCGAAAAAAGATGATTGGAATGAAGAACCGAGGATCAAAAGAAAAAATGTTCTATT  
TTCTCTATAAAGGAGAGATGAGCCAGGAGATATTTTGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA  
AGAAGCTGGTGGTGGTGGTGGTTCCTTTCTTTTGAATTTCCCACAAGAGAGAGGAATTAATAATACATCTG  
AARGAATTTAGAGAGAAAAAGTTGACCCGGCGAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCA  
CAGTTGGATTTTGTGCCTATGTTGACTAAATGACGGATAAATGCAGTTGGATTTTCTTCATCAACCTCTCTT  
TTTTTAAATTTTTTATCTTTTGGTATCAAGATCATGCGGTTTCTCTGTGTTCAACCACTGGATTTCCATCT  
GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACCAGATAAAATATGAATG  
TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTAGGTTTAACAGGGCCCTATTGACCCCT  
GCTTGGTGGTGTGCTGCTGCTCTTCAACTTCTTGTGGTGGCTGGTCTGTGTCGGGCTCAGACCTGCCCTTCTGTGT  
GCTCCTGCAGCAACCGATTGACGAAGGTTGATTTGTTCGGAAAAACCTCGCTGAGCTTCGGATGGCATCTCC  
ACCAACACACCGCTGCTGAACCTCTCATGAGAACCAATCCAGATCATAAAGTGAACAGCTTCAAGCATCTGAG  
CGATCTGGAATTCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGTTCTGGCGA  
ACCTCAACACTCTGGAACCTTTGACAACTCGTCTTACTACCATCCCGAATGGAGCTTTGTATACTTGTCTAA  
CTGAAGGAGCTCTGGTTGCGAAACAACCCCATGAAAGCATCCCTCTTATGCTTTTAAACAGAATTCCCTCTTT  
TGGCCGACTAGACTTAGGGGAATTGAAAAGACTTTTCATACATCTCAGAAGTGGCTTTGAAGGCTGTGCTCAACT  
CGAGTATTTGAACCTTGCCATTGCAACCTTCGGGAATCCCTAACCTCACACGCTCATATAAATAGATGAG  
CTGATCTTCTTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTCCAGGTTTGTATGCACCTTCAAAACT  
GTGGATGATACAGTCCAGATTCAAGTGATTGAACCGAATGCCTTTGACAACTTCAGTCACTAGTGGAGATCA  
ACCTGGCACAACAATAATCTAACATTACTGCCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGAGGATCAT  
TTACATCAACAACCTTGGAACTGTAAGTGTGACATCTGTGGCTGAGTGGTGATGAGTAAAGACATGGCCCCCTC  
GACACAGCTGTTGTGCGCGGTGAACACTCTCCCAATCTAAGGGGAGGTGATCATGGAGGCTCGACCAGA  
ATTACTTCACGCTGATGCTCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT  
GAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGAACAGTCTATGACACA  
TGGGGCGTACAAAGTGGGATAGCTGTGTCAGTGATGGTACGTTAAATTTCACAAGTGAAGTGTGCAAGAT  
CAGGCATGTACACATGTATGTGAGTAATTCGTTGGGAATACTGCTTGCAGACCCCTGAATGTACTGCA  
GCAACCTACTACTCTTTCTCTTACTTTTCAACCGTCAGATAGAGACTATGGAACCGTCTCAGGATGAGGCAG  
GACCACAGATAACAATGTGGTCCCCTCCAGTGGTGCAGTGGGAGACCACCAATGTGACCACTCTCTCACAC  
CACAGAGCACAAGTGTGACAGAGAAAACTTCAACATCCAGTGACTGATATAAACAGTGGGATCCAGGAAT  
GATGAGTCTGAAGACTACCAAAATCATCATTTGGGTGTTTGTGGCCATCAGCATGAGTGCAGTGTGCT  
GGTCATTTTCTACAAGATGAGGAAGCAGACCACTGCTTAAACCAACCTCACGCCCCACAGGACTGTTGAAATTA  
TATATGTGGATGATGAGATTACGGGAGACACACCCATGGAAGGCCACCTGCCATGCTGTCTCGAGCATGAG  
CACCTAAATCACTATAACTCATACAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTCATACACA  
CAGTTCAGTGCATGAACGTTATTGATCGAATGAACCTTAAGACAAATGTACAAGAGACTCAATCTAAACA  
TTTACAGAGTTACAAAAACAACAATCAAAAAAAGACAGTTTATTAATAAATGACACAATGACTGGGCTAA  
ATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACAAGAAAGAAATTTATTTATTAATAATCTTATTG  
TGATCTAAGACGACAAAAA

**FIGURE 314**

MLNKMTLHPQQIMIGPRFNRLFDPLLVLLALQLLVVAGLVRAQTCPSCSCSNQFSKVIC  
 VRKNLREVPDGISTNTRLNLHENQIQIIVNSFKHLRHLEILQLSRNHRTIEIGAFNGLA  
 NLNTLELFDNRLTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRDLGELKRLS  
 YISEGAFEGLSNLRYNLAMLNLRREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL  
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL  
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
 LKCRASLTLSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTVQDTGMYTCMVSNSVGN  
 TTASATLNVTAATTTTFSYFSTVTIVETMEPSQDEARTDNNVVGPTPVVDWETTNVTTSLTPQ  
 STRSTEKTFITIPVTDINSIGPGIDEVMKTKIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
 HHAPTRTVEIINVDDTEITGDTFMESHLMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
 VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,  
 434-438, 442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
 391-397, 422-428, 433-439, 531-537

**FIGURE 315**

GCGCCGGAGCCCATCTGCCCCAGGGGCACGGGGCGGGGGCCGGCTCCCGCCCGGCACAT  
 GGCTGCAGCCACCTCGCGCGCACCCTGAGGCGCGCGCCAGCTCGCCCGAGGTCCGTCCGA  
 GCGCGCCGGCGCGCCCGGAGCCAAAGCAGCAACTGAGCGGGGAAGCGCCGCGCTCCGGGGGATC  
 GGGATGTCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACTTTGGGGACTCA  
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCACTGGGGC  
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCAAAAA  
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
 AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC  
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCCGTACGTGTGGAGCCAT  
 GTCATCTTAAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
 AGAAGGAAGTGACTGACTTTGCAGTGTGAGTCACTCTGGCACAGAGCCCATTTGTGTATT  
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAATCTAGGATT  
 GACTACAACCACCTTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTTACTCTGGACTGTA  
 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGGCAGTAAGTGTACAGT  
 ATGTACAAAGCATCCGGATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATGAGGAAGAAGA  
 GAGACCTAATGAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAACCCAGCT  
 CCTCTTCTCCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAT  
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC  
 CCAGGCTACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG  
 CTAATCTGACCAAGCAGAAACCACACCCAGCATGATCCCGAGCCAGAGCAGACCTTCCAA  
 ACGGTCTGAATTACAATGGACTTGACTCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC  
 TTCTCGTCATTGGAGCTCAAGTCACCAAGCCACCAACCAGATGAGAGGTCATCTAAGTAGCA  
 GTGAGCATTGCACGGAACAGATTAGATGAGCATTTTCTTATACAAATACCAACAGCAAA  
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTCCTTATAGACCAGAGTAAGGG  
 AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAGGTTG  
 AGGTGAATATACCTAAAACTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAAATT  
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAACTATTGGGATT  
 ATTAGTTATTAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
 TGAGCTAACCACCTTCAAGAAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
 TTCATTGTGTCATAAGGTTTGGATATTAAATTCAAGGGGAGTTGAATAGTGGGAGATTGGAGA  
 AGAGTGAATGAGTTTCTCCACTCTATACATACTCTACTATTTGATTAGGCCAAAATAAC  
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCTGATGTT  
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCAAT  
 CAGATGGCTCTAAGGACTTTCTGCTAGATATTCTGGAAGGAGAAAAATACAACTGTCAATT  
 TATCAAGCTCTCTAGAAAGAAATCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
 CCCAACATACCATTTATAGTCTCTTCTTCTGAGAAAAATGTGAACAGGAATTGCAAGACTGG  
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
 TGGTGCCAGCACTGTAGGAATAATCCAGCAGGTGGAGGTTGCACTGAGCCGAGATTATGCC  
 ATTCACCTCCAGCCTGGGTGAACAGAGCGGGACTCCGTCTC

**Don't miss it!**

**Don't miss it!**

**Don't miss it!**

[illegible]

**Don't miss it!**

**Don't miss it!**

**Don't miss it!**

[illegible]

**Don't miss it!**

**FIGURE 317**

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCGCCTACCTGCAGCCGCGGCCACGGCAGCGCAGCCA  
 CCA**ATG**CGCGCTCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTCGCCACAAGATTGTAGATCACTACT  
 CCTGAAGCATGATTGAAAAAGCCAAAGGGGAACTGCCTATCTGCCATGCAAAATTTACGCTTAGTCCCGAAGA  
 CCAGCGACCGCTGACACATCCAGTGGCTGATATCACAGCTGATAATCAGAAGCTGGATCAAGTGATTATTTTAT  
 ATCTGGAGCAAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTAGCTTTACGAGTAATGATCTC  
 AAACTCTGCTGATGCATCAATAAATGTAAACGAATTTACAACCTGTCAGATATTGGCCACATATCAGTGCAAAAGTAA  
 AAAAGCTCCTGTGTTGCAAAATAAGAAGATTCACTGGTAGTCTTGTTAAGCCTTCAGGTGCGAGATGTTACG  
 TTGATGGATCTGAAGAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCACTTCCATTACAG  
 TATGAGTGGCAAAAATTTGCTGACTCACAGAAAAATGCCACTTCATGGTACAGAAACAGAGTGGGCTCTGATC  
 ATCTGTAAAAAATGCCTCTCTGAGTACTCTGGGACATACAGCTGTACAGCTCAGAAACAGAGTGGGCTCTGATC  
 AGTGCCTGTTGCGCTCAAAACGTTGTCCTCCTTCAAATAAAGCTGGACTAATTTGCAGGAGCCATTATAGGAAC  
 TTGCTTGTCTAGCGCTCATTTGGTCTTATCATCTTTTGTCTGTGTAAGAGCGCAGAGAAAGAAAAATATGAAA  
 GGAAGTTCATCAGCATATCAGGGAAGATGTGCCACCTCCAAGAGCCGTCAGTCCATGCCAGAGCTACATCG  
 GCAGTAATCATTCATCCCTGGGTCATGTCTCCTTCCAACATGGAAGGATATTCCAAGACTCAGTATAACCAA  
 GTACCAAGTGAAGACTTTGAACGCACTCCTCAGAGTCCGACTCTCCCACTGCTAAGTTCAGTACCCCTTACAA  
 GACTGATGGAATTACAGTTGTAT**TAAAT**ATGGACTACTGAAGATCTGAAGTATTGTATTATTGACTTTATTTT  
 AGGCCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGAGCAGCTGAAGAACAC  
 ATCTACTTTATGCAATGGCATTTAGACATGTAAAGTCAGATGTCATGTCAAATTTAGTACGAGCCAAATTTCTTGT  
 TAAAAAACCTATGTATAGTGACACTGATAGTTAAAGATGTTTTATTATATTTTCAATAACTACCCTAACAA  
 ATTTTAACTTTTCATATGCATATTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAAATAGTTGATTTTCAA  
 AGGAATTTTAAATTTCTACGTTCTGTTTAAATGTTTTGCTATTAGTTAAATACATTTGAAGGGAATACCCG  
 TCTTTTTCCCTTTTATGCACACAACAGAAACACGCGTTGTCATGCCCTAAAATTTTTTTTATTTGCAACTACA  
 TGATTTTCAACACATTTCTTTAAACACGACATAAAATAGATTTCCTTGATATAAAATACTTACATACGCTCCA  
 TAAAGTAAATTTCTCAAAGGTGCTAGAACAATCGTCCACTTCTACAGTGTCTCGTATCCAACAGAGTTGATGC  
 ACAATATATAAATCATCAAGTCCAATATTTAAAACTTAGGCACCTGACTAACTTTAATAAAATTTCTCAAATA  
 TATCAATATCTAAAGTACATATATTTTAAAGAAAGATTATTCTCAATAACTTCTATAAAATAAGTTGATGG  
 TTTGGCCCATCTAACTTCACTACTATTAGTAAAGACTTTTAACTTTTAAATGTGTAGTAAAGGTTATTCTACCTT  
 TTTCTCAACATGACCAACACCAATCAAAACGAAAGTTAGTGAGGTGCTAACTATGTGAGGATTAAATCCAGTGAT  
 TCCGGTCAATGCAATCCAGGAGGAGGTACCCATGTCACGTGGAATTTGGCGATATGGTTTATTTTCTCTCCC  
 TCATTTGGATAACCAAATGGAACAGGAGGAGGTAGTGATTCTGATGGCCATTCCCTCGATACATTCTCTGGCTT  
 TTTTCTGGGCAAGGTTCCACATATGGAAGAGGTGCAAAATATAGTTCGAAATCTGTAGGGAAGAGAACATAT  
 TAGTTTAATTCAGAAAGAAAAATCATCATCTATGTTCCAGATTCTCATTAAGACAAAGTTACCCACAACAT  
 GAGATCACTATCAAGTGACACTCCTATGTCTCAGGTCTAAATACATTAATAAACCCTCATGTGTAATAGGCGTATAA  
 TGTATACAGGTTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAAATCAACACAGTACTCTCTTAACAA  
 CTTCAACCAAAAAGACAAAAACATGGAAACGAATGGAAGCTTTGTAAAGCATGCTTGTTTTATGCTCCAGTGGTT  
 CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAACATTTGAGCTGGAGCGCTATATCTCTT  
 AGCAAACTAATGCAGAAACAGAAATCAACTACCGCATTTCTCACTATAAGTGGGAGTAAATGATAGAACT  
 TATGAACCAAAAGAGGAAACAATAGACATTTGGAGTCTATTTGAGAGGGGAGGGTGGGAGGAGAAAGAGCA  
 GAAGAAGATAACTATTGTAGTCTGCCTTCAACCTGGGTGATGAATATATGTACACAAATCCCTGTGCACACA  
 TGTTTACCTATGGAACAAACCTTCATGTGATCCCTAAACCTAAAATAAAGTTAAAAA  
 AA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

0969725-11201

**FIGURE 318**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA  
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVNLQLSDIGTYQCKVKK  
APGVANKKIHLVVLVKPSGARYVDGSEEIGSDFKIKCEPKESLPLOYEWQKLSDSQKMPT  
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPPSNKAGLIAGAIIGTLL  
ALALIGLIIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM  
EGYSKTQYNQVPSDFERTPQSPTLPPAKFKYPYKTDGITVV

**Signal sequence.**

amino acids 1-19

**Transmembrane domain:**

amino acids 236-257

**N-glycosylation sites.**

amino acids 106-110, 201-205, 298-302

**Tyrosine kinase phosphorylation sites.**

amino acids 31-39, 78-85, 262-270

**N-myristoylation sites.**

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,  
245-251, 296-302

**Myelin P0 protein.**

amino acids 96-125

**FIGURE 319**

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCTCTGATTGGTGA  
 ATGGTGAAAGTGCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC  
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC  
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG  
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC  
 CTTTGTCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCTG  
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT  
 GAAGGGGGTTGTTCCCCAGAAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG  
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT  
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAACCTGTTTTCAAAAA  
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAT  
 TTGTTCTCATCGTGTCAACATGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC  
 AGTGCACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAAACAGTTGGACGTAGAAGCAGC  
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATCTACAAGC  
 TCTGAATGCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTTCA  
 AACAGTCTCCCTTCCATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCT  
 TTGGCCCAGGATTATTGTCAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG  
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATATTATTACAACCTATTTT  
 AATTAATGTCAGTATTTCAACTGAAGTTCATTTATTGTTGAGACTGTAAGTTACATGAAGG  
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCTCACAACTCTTGCCACAGTGTGGGGCAG  
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGTCTTTTTTGGCCTGTCTTTGGATT  
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACT  
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAAAG  
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT  
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCCTTTTTTTTT  
 TATCCTAGTCATTCTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC  
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATCCCTGTCTAATAAAAGACAACATAA  
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 320**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTILLWSQVSGAQGQEFHFGPCQVK  
GVVPQKLWEAFWAVKDTMQAQDNITSARILLQQEVLQNVSDAESCYLEVHTLLEFYLLKTVFKNH  
HNRTVEVRTLKSESTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL  
TKALGEVDILLTWMQKFYKL

**Signal sequence:**

amino acids 1-42

**N-glycosylation sites.**

amino acids 85-89, 99-103, 126-130



**FIGURE 321**

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC  
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC  
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG  
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA  
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA  
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTCTCTACA  
TGCAGAAAACCTCTGCGGCAATGTCAAGAACAGAGGCAGTGCTCACTGCAGGCAGGAAGCCACC  
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTTGCTGCGGTTTACT  
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGTGAAGGTC  
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAATAGGCAAAAAGTCTACTGTGGTAT  
TTGTATAAACTCTATCTGCTGAAAGGGCTGCAGGCCATCCTGGGAGTAAGAGGCTGCCTT  
CCCATCAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
GTAGTACAAATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTACCTATGA

**FIGURE 322**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282  
><subunit 1 of 1, 177 aa, 1 stop  
><MW: 20452, pI: 8.00, NX(S/T): 2  
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVITILST  
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANFLYMQKTLRQCQEQ  
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

**Signal sequence:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 56-60, 135-139

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation site.**

amino acids 24-30

**Actinin-type actin-binding domain signature 1.**

amino acids 159-169

**FIGURE 323**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG  
 AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT  
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACTGCACCTC  
 GGTTCATATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACG**ATGT**TGGGGGCCCGCCT  
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA  
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC  
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC  
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA  
 TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTTGGATCACACTATTCGAC  
 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC  
 TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC  
 CACCCCGTACTCCAGTTCCCTGTCCCGAGGAACGAGATCCCCCTAATTCACTTCAACACC  
 CCCATACCACGGCGGCACACCCGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT  
 GCTGAAGCCCGGGCCCGGATGACCCCGGCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG  
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGCGGTCGAGTGAAC  
 ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATC**TAG**GGTGC  
 CTGG

**FIGURE 324**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238
```

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRRLVWCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLTYTATARNSYHLQIHKNGHVD  
GAPHQTIYSALMIRSEDAGFFVITGVMSRRYLCDMFRGNI FGSHYFDPENCRFQHQTLNGY  
DVYHSFPQYHFLVLSGRAKRAFLPGMNPFPYSQFLSRNREIPLIHFNTPIPRRHTRSADDSE  
RDLNVLKPRA RMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGTGPEGCRPFA  
KFL

Important features of the protein:

Signal peptide:

amino acids 1-24

## cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

## HBGF/FGF family proteins

amino acids 73-124

**FIGURE 325**

GGAAAGGTTACCCGCGAGAGACAGCCAGCTTCTGTGGAGCAGCGGTGGCCGGCTAGGATG  
GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG  
GAGCTCTGCAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAA CGGACGACACAGAAG  
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGTCTGGAACCTCAAACGCTGAGCGCTGAG  
ACCTCTTCTAGGGCTCAACCCAGCCGGGCCCATTTCCAGAAGCAGAGACAGGGGAGGCCAA  
GAGAAATTTCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCACTTCATGTTGC  
TGATCGCCACCTCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC  
ACAGTTCAGACCATCAGAGGCAGTGATCCGAGGAAGCCATCTTTGACACCTTTGCACCCGA  
TGACAGCTCTGAAGAGGCAAAGACACTCACAAATGGACATATTGACATTGGCTCACACCTCCA  
CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC  
ACCCCGTACAGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCC  
GTACAGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCCCTCAT  
GGTCCCCGGGACTGATGTCCTCTCTCGCTGAAGCCCTTGTGACTGTCACAAACCTCGAG  
GTTATTAATTGCAGCATCACAGAAATAGAAACAACCACTTGCAGCATCTCCCTGGGGCTCAGA  
CATGATCTCATCCCCCAGGAAGGGGTGAAGGCTCTGTCACACTCCGATCCACCAGCTCTGC  
CTGACTTCACTGAAGCAAAACCACATCACTGAGGTCACAGCCTCTGCCGAGACCTGTCC  
ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA  
CAGCGCCACAGAAAGAGAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA  
CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC  
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGACAGTGGGCAAAACAACCTC  
CTTTGCTGGGAGCTCTGCTTCTCTTACAGCCCCCTCGGAAGCCGCCCTCAGAACCTTCAACC  
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCTT  
CTTCTTCTGTCTCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA  
GATCACAACTCAGCGAAGACCAGATGAAGCCCCAACAGCCACGCCACGCCACGACTGCCCGGAC  
GAGGCCGACCACAGACCTGAGTGTCAGGTTGAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG  
TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC  
CGGGAACCTCCACGCCACGCGCTCACTTCCAGGTCTCTTACTGCGTGTGAGGAGAGGCTA  
ACGGACATCAGCTGCAGCCAGGCATGTCCTGATGCCAAAAGAGGGTGTGCCCCTAGCCTG  
GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCATG  
AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCTCGCTCATATCCAC  
CGGAGTGTATGATGGGAGGGGTTACCTGTTCCAGAGGTGTCCTTGGACTACCTTGG  
CATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCATCTGTGTGCTTCCATCTGCA  
TTAAATTAACCTGAGCTGGCCCAAAAAAAA

**FIGURE 326**

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLSA  
 ETSSRASTPAGPIPEAETRGAKRISFARETRSFKTSPNFMVLIATSVETSAASGSPEGAGM  
 TTVQITITGSDPEEAI FDTLCTDDSSEEAKLTMDILTIAHTSTEAKGLSSESSASSDGPHPV  
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLEALVTVTNI  
 EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL  
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALS VETPSY  
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYPSEAAALKNFTPSETPTMDIATKGPFPTSRD  
 PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT

**N-glycosylation sites:**

amino acids 252-256, 445-449, 451-455

**cAMP-and cGMP-dependent protein kinase phosphorylation site.**

amino acids 84-90

**Casein kinase II phosphorylation sites.**

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,  
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,  
 404-408, 414-418, 431-435

**N-myristoylation sites.**

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-  
 320, 349-355, 386-392, 397-403, 449-455

**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

**FIGURE 327**

GCGGAGCATCCGCTGCGGTCTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTCTCCGCGGG  
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA  
 GAGAGAAATCTCATCTGTGCGACCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT  
 CCTTGACCTTTGAAGACCAAACCTAAACTGAAATTTAAATGTTTCTTCGGGGGAGAAGGGAG  
 CTTGACTTACACTTTGGTAATAATTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTTTCTAAGGGAATC  
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTTCAC  
 AAAAAACATATCAGGGGACAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA  
 GACAACCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACAGCA  
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAATTTTCAAGCAGTCACTCCCC  
 TAGCCCATCATCACAGATTATTCAAAGCCACCAGATATCTCATGGAGAGACACACTTTCT  
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA  
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTCACAATTTTCTCTGATCAAGAAA  
 TAGCTCATCTGCTGCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
 CATACCACCTCGGCTACTCCAAGGCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC  
 TTCTGGGACTTCCAGGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
 AGCCTCCCACGACCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG  
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCTA  
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCCTGGGAAGGT  
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCCAGAAAACTCAGTACGGCCTTCC  
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGGTGCTCTGTTCTGGTGATAGGCC  
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT  
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTGCTGTCTCTTAATTCATT  
 TAGTAACCAAGGCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG  
 TATTTTGAAGACAGGAAAAATGCCCTTCTGCTTTCTCTTTTTTTTTTTGGAGACAGAGTCTT  
 GCTCTGTTGGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCACAACCTCCGTCTC  
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
 CCACACCTGGGTGATTTTTGTATTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG  
 GTCCTAAATCCTGACCTAGTGATCCACCTCCTCGGCTCCCAAAGTGTCTGGGATTACAGG  
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGAAGGAATGAAGT  
 GGAACCAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATAGCTAAAAACAAGAGCTCT  
 ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA  
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATTCCTGGTTCAGATAAAATCAAC  
 GTTTTTATCAATTTCTAATGGATTGCTTTCTTTTATATGGATTCTCTTTAAACCTTATT  
 CCAGATGTAGTTCCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

**FIGURE 328**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVVICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLHLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAATLQAMATTAVLTTFQAP
TDSKGSLETIPFTEISNLTNLNTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFKEKWLIGSLLFGVFLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI
```

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321



**FIGURE 329**

CTCCACGGTGTCCAGCGCCCA**AATG**CGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT  
 CCCAGGTTATGAAGCCTTGGAGGGCCAGAGGAAATCAGCGGGTTTCGAAGGGGACACTGTGT  
 CCTCGAGTGCACCTCAGGGAAGAGCTGAGGGACACCAGGAAGTACTGGTGCAGGAAGGTT  
 GGGATCCTCTCTCTCGTCTGCTTGGCACCATCTATGCAGAAGAAGGCGCAGGACAAAT  
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGTGACCCCTGTGGA  
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAACCGGGGCCCCGATGAG  
 TCTTTACTGATCTCTCTGTTTCGTCTTTCCAGGACCCCTGCTGTCCCTCCCCTCCCCTTCTCCCAC  
 CTTCCAGCCTCTGGCTACAACACGCTGACAGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC  
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGACAGGGAGCTCCCGCCCCCCTATGCAGC  
 TGGACTCCACCTCAGCAGAGGACACCAAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCCAGG  
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTGCTGAGCCCTTCTGTGAGC  
 CGCAGGCCCTGATCGCCTTCTGACGCCACCTGCTCCTGTGGAGAAAGCAAGCTCAACAGGCCA  
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTCGGAGGAAAAGGAAGCC  
 CTTTCCAGGCCCTGAGGGGACGTGATCTCGATGCTCCCTCCACACATCTGAGGAGGA  
 GCTGGGCTTCTCGAAGTTTGTCTCAGCG**TAG**GGCAGGAGGCCCTCTGGCCAGGCCAGCAGT  
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
 TCCAGCTGCCCGGACTCAGGGGCTCTCCCAACCTCCCGAGGCTCTCCTCTTGATCTTCCA  
 GCTTGACCTAGAAAGCGTTTGTGAGCCCTGGAGCCCCAGAGCGGTGGCCTTGCTCTCCGGCTG  
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA  
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGCTTGAGTTTCAATCTGCCAGGAACTCCTGGGC  
 CTCATGCCCAGTGTGCGACCCCTGCCTTCCCTCCACTCCAGACCCCACTTGTCTTCCCTCCC  
 TGGCGTCTCTCAGACTTAGTCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT  
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAGGAAGCCT  
 GTGAAAAACGTGATTCTCTGGCCCCACCAAGACCCACCAAAAACATCTCTGGGCTTGGTGCAG  
 GACTCTGAATTTCTAACAATGCCCAGTGACTGTGCGACTTGAGTTTGGAGGCCAGTGGGCCGTG  
 ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGCTCTCCACCTGCC  
 CAATAGATCTGCTCTGCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG  
 TCCAGGCCTTGGTCAGGTCAGGTGCACATTCAGGATAAGCCAGGACCGGCACAGAAGTGG  
 TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCTTTGGAAAAAATGATGAAGA  
 AAACCTTTGGCTCCTTCTCTGTCTGAAAGGGTTACTTGCTATGGGTTCTGGTGGCTAGAGA  
 GAAAAGTAGAAAACACAGAGTGACGTAGGTGTCTAACACAGAGAGAGTAGGAACAGGGCGG  
 ATACCTGAAGGTGACTCCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA  
 GCACAACACTATTTTTTTTCTTTTCCATTATTATTGTTTTTAAAGCAGAACTCTCGTGTCT  
 GCTGCCACTGAGGTGGAGTGGCAGCATCTGCAAACTCCGCCCTCCTGGGTTCAAGTGATT  
 CTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACACCTGGCTAATT  
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC  
 CTCAAATGAGCCTCCTGCTTCACTCTCCAAATTGCCCGGATTACAGGCATGAGCCACTGTG  
 TCTGGCCCTATTTCTTTTAAAGAGTGAATTAAGAGTTGTTCAGTATGCCAAAACCTGGAAG  
 ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCATAGTCTCACCAGACATATCAT  
 TATTTTCGTTTGTGTGACTTCTCTCCACTCTTTTCTTCTTACATAAATTGCGCGTGTCTTT  
 TTTACAGAGCAATTATCTTGATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
 ATCACTTTATTCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAATGTTCTATCA  
 GCTGCATAAAAAAAAAAAAAA

**FIGURE 330**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLQDAGEYWCVEKRGPDSELLISLFV  
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEPPLPG  
TSQYGHERTSQYTGTSPPHATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
LAPVLVLLSLLSAGLIAFCSHLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD  
VISMPLHTSEEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128